

Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Lys Glu
930 935 940

Leu Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu
945 950 955 960

Val Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro Asn Asp Ser
965 970 975

Lys Phe Phe Gln Asn Leu Leu Asp Glu Glu Asp Leu Glu Asp Met Met
980 985 990

Asp Ala Glu Glu Tyr Leu Val Pro Gln Ala Phe Asn Ile Pro Pro Pro
995 1000 1005

Ile Tyr Thr Ser Arg Ala Arg Ile Asp Ser Asn Arg Ser Glu Ile
1010 1015 1020

Gly His Ser Pro Pro Pro Ala Tyr Thr Pro Met Ser Gly Asn Gln
1025 1030 1035

Phe Val Tyr Arg Asp Gly Gly Phe Ala Ala Glu Gln Gly Val Ser
1040 1045 1050

Val Pro Tyr Arg Ala Pro Thr Ser Thr Ile Pro Glu Ala Pro Val
1055 1060 1065

Ala Gln Gly Ala Thr Ala Glu Ile Phe Asp Asp Ser Cys Cys Asn
1070 1075 1080

Gly Thr Leu Arg Lys Pro Val Ala Pro His Val Gln Glu Asp Ser
1085 1090 1095

Ser Thr Gln Arg Tyr Ser Ala Asp Pro Thr Val Phe Ala Pro Glu
1100 1105 1110

Arg Ser Pro Arg Gly Glu Leu Asp Glu Glu Gly Tyr Met Thr Pro
1115 1120 1125

Met Arg Asp Lys Pro Lys Gln Glu Tyr Leu Asn Pro Val Glu Glu
1130 1135 1140

Asn Pro Phe Val Ser Arg Arg Lys Asn Gly Asp Leu Gln Ala Leu
1145 1150 1155

Asp Asn Pro Glu Tyr His Asn Ala Ser Asn Gly Pro Pro Lys Ala
1160 1165 1170

Glu Asp Glu Tyr Val Asn Glu Pro Leu Tyr Leu Asn Thr Phe Ala
1175 1180 1185

Asn Thr Leu Gly Lys Ala Glu Tyr Leu Lys Asn Asn Ile Leu Ser
1190 1195 1200

Met Pro Glu Lys Ala Lys Lys Ala Phe Asp Asn Pro Asp Tyr Trp
1205 1210 1215

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Asn His Ser Leu Pro Pro Arg Ser Thr Leu Gln His Pro Asp Tyr
1220 1225 1230

Leu Gln Glu Tyr Ser Thr Lys Tyr Phe Tyr Lys Gln Asn Gly Arg
1235 1240 1245

Ile Arg Pro Ile Val Ala Glu Asn Pro Glu Tyr Leu Ser Glu Phe
1250 1255 1260

Ser Leu Lys Pro Gly Thr Val Leu Pro Pro Pro Tyr Arg His
1265 1270 1275

Arg Asn Thr Val Val
1280

<210> 101

<211> 623

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 101

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Thr Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
145 150 155 160

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
165 170 175

Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
180 185 190

Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val
 195 200 205
 Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys
 210 215 220
 Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly
 225 230 235 240
 Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys
 245 250 255
 Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met
 260 265 270
 Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn
 275 280 285
 Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu
 290 295 300
 His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr
 305 310 315 320
 Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His
 325 330 335
 Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser
 340 345 350
 Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr
 355 360 365
 Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys
 370 375 380
 Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp
 385 390 395 400
 Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg
 405 410 415
 Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro
 420 425 430
 Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser
 435 440 445
 Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val
 450 455 460
 Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln
 465 470 475 480
 Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro
 485 490 495

Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
500 505 510

Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg
515 520 525

Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu
530 535 540

Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr
545 550 555 560

Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn
565 570 575

Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp
580 585 590

Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln
595 600 605

Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
610 615 620

<210> 102

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 102

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195 200 205

Leu Cys Lys Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn
210 215 220

Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly
225 230 235 240

Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala
245 250

<210> 103
<211> 628
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 103

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser

145 150 155 160
 His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
 165 170 175
 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 180 185 190
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val
 195 200 205
 Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Ala Glu
 210 215 220
 Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala
 225 230 235 240
 Leu Leu Val Val Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys
 245 250 255
 Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser
 260 265 270
 Glu Arg Asn Asn Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn
 275 280 285
 Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn
 290 295 300
 Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe
 305 310 315 320
 Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr
 325 330 335
 Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu
 340 345 350
 Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg
 355 360 365
 His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly
 370 375 380
 Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro
 385 390 395 400
 Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met
 405 410 415
 Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser
 420 425 430
 Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr
 435 440 445
 Val Ser Met Pro Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg
 450 455 460

Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp
465 470 475 480

His His Pro Gln Gln Phe Ser Ser Phe His His Asn Pro Ala His Asp
485 490 495

Ser Asn Ser Leu Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu
500 505 510

Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys
515 520 525

Leu Ala Asn Ser Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile
530 535 540

Ala Asn Arg Leu Glu Val Asp Ser Asn Thr Ser Ser Gln Ser Ser Asn
545 550 555 560

Ser Glu Ser Glu Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe
565 570 575

Leu Gly Ile Gln Asn Pro Leu Ala Ala Ser Leu Glu Ala Thr Pro Ala
580 585 590

Phe Arg Leu Ala Asp Ser Arg Thr Asn Pro Ala Gly Arg Phe Ser Thr
595 600 605

Gln Glu Glu Ile Gln Ala Arg Leu Ser Ser Val Ile Ala Asn Gln Asp
610 615 620

Pro Ile Ala Val
625

<210> 104

<211> 252

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 104

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu

85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195 200 205

Leu Cys Lys Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn
210 215 220

Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly
225 230 235 240

Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala
245 250

<210> 105
<211> 637
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 105

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Thr Gly Thr
165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195 200 205

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
210 215 220

Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val
225 230 235 240

Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met
245 250 255

Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His
260 265 270

Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn
275 280 285

Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln
290 295 300

Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile
305 310 315 320

Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser
325 330 335

Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp
340 345 350

Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile
355 360 365

Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly
370 375 380

Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser
385 390 395 400

Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro

405 410 415
His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser
420 425 430
Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu
435 440 445
Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala
450 455 460
Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro
465 470 475 480
Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser
485 490 495
Ser Phe His His Asp Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser
500 505 510
Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr
515 520 525
Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala
530 535 540
Lys Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp
545 550 555 560
Ser Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp
565 570 575
Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu
580 585 590
Ala Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg
595 600 605
Thr Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg
610 615 620
Leu Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
625 630 635

<210> 106

<211> 260

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 106

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys
1 5 10 15
Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195 200 205

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
210 215 220

Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Arg
225 230 235 240

Asn Ser Gly Lys Ser Cys Met Thr Val Phe Gly Arg Ala Phe Gly Leu
245 250 255

Asn Glu Thr Ile
260

<210> 107
<211> 620
<212> FRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 107

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45
 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
 Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125
 Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140
 Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
 145 150 155 160
 His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
 165 170 175
 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 180 185 190
 Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val
 195 200 205
 Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu
 210 215 220
 Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
 225 230 235 240
 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp
 245 250 255
 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile
 260 265 270
 Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu
 275 280 285
 Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val
 290 295 300
 Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr
 305 310 315 320
 Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser
 325 330 335

Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile Val
340 345 350

Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro
355 360 365

Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe
370 375 380

Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His
385 390 395 400

Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
405 410 415

Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met
420 425 430

Ser Pro Pro Val Ser Ser Met Thr Val Ser Lys Pro Ser Met Ala Val
435 440 445

Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro
450 455 460

Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser
465 470 475 480

Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro
485 490 495

Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu
500 505 510

Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys
515 520 525

Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser
530 535 540

Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu
545 550 555 560

Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala
565 570 575

Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr
580 585 590

Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln Ala Arg Leu
595 600 605

Ser Ser Val Ile Ala Asn Gln Asp Pro Ile Ala Val
610 615 620

<210> 108

<211> 251

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 108

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
 145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
 195 200 205

Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
 210 215 220

Val Met Ala Ser Phe Tyr Arg Asn Ser Gly Lys Ser Cys Met Thr Val
 225 230 235 240

Phe Gly Arg Ala Phe Gly Leu Asn Glu Thr Ile
 245 250

<210> 109

<211> 224

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 109

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140

Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
 145 150 155 160

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
 165 170 175

Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 180 185 190

Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val
 195 200 205

Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 210 215 220

<210> 110

<211> 194

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 110

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30

Pro Ala Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala

35 40 45
 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95
 Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110
 Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125
 Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140
 Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Gly Thr Ser
 145 150 155 160
 His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
 165 170 175
 Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
 180 185 190
 Cys Lys
 <210> 111
 <211> 224
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 111
 Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
 1 5 10 15
 Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45
 Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60
 Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80
 Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
145 150 155 160

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
165 170 175

Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
180 185 190

Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val
195 200 205

Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
210 215 220

<210> 112

<211> 445

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 112

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130 135 140

Gly Ala Tyr Val Ser Ser Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser
145 150 155 160

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly
165 170 175

Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
180 185 190

Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val
195 200 205

Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys
210 215 220

Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly
225 230 235 240

Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys
245 250 255

Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met
260 265 270

Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn
275 280 285

Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu
290 295 300

His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr
305 310 315 320

Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His
325 330 335

Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser
340 345 350

Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr
355 360 365

Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys
370 375 380

Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp
385 390 395 400

Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg Arg Asn
405 410 415

Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His
420 425 430

Leu Arg Ser Ser Ser Ile Pro His Leu Gly Phe Ile Leu
435 440 445

<210> 113
 <211> 252
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product

<400> 113

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Lys Lys
 1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
 35 40 45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
 50 55 60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
 65 70 75 80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
 85 90 95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 100 105 110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
 115 120 125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
 130 135 140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
 145 150 155 160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
 165 170 175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
 180 185 190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
 195 200 205

Leu Cys Lys Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn
 210 215 220

Arg His Leu His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly
 225 230 235 240

Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys Ala Ala
 245 250

<210> 114
 <211> 539
 <212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 114

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Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
1      5      10      15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
20     25     30

Pro Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala
35     40     45

Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser
50     55     60

Ser Leu Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys
65     70     75     80

Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu
85     90     95

Leu Arg Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
100    105    110

Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr
115    120    125

Ile Val Glu Ser Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu
130    135    140

Gly Ala Tyr Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr
145    150    155    160

Glu Gly Ala Asn Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr
165    170    175

Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
180    185    190

Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
195    200    205

Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
210    215    220

Val Pro Met Lys Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln
225    230    235    240

Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val
245    250    255

Gly Ile Met Cys Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys
260    265    270

Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn
275    280    285

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Met Met Asn Ile Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu
290 295 300

Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser
305 310 315 320

Glu His Ile Val Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His
325 330 335

Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser
340 345 350

His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His
355 360 365

Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro
370 375 380

Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu
385 390 395 400

Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg
405 410 415

Asp Ser Pro His Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
420 425 430

Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
435 440 445

Pro Ser Glu Met Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro
450 455 460

Ser Met Ala Val Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu
465 470 475 480

Val Thr Pro Pro Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln
485 490 495

Gln Phe Ser Ser Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu
500 505 510

Pro Ala Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr
515 520 525

Gln Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys
530 535

<210> 115

<211> 1180

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 115

Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu

1 5 10 15
 Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30
 Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45
 Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60
 Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80
 Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95
 Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110
 Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125
 Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140
 Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160
 Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175
 Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300
 Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
 305 310 315 320

Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
325 330 335

Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
340 345 350

Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
355 360 365

Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
370 375 380

His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
385 390 395 400

Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ile Asn Asp Cys
405 410 415

Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys Arg Asp Leu Val Asn Gly
420 425 430

Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala Gly Asp His Cys Glu Arg
435 440 445

Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys Leu Asn Gly Gly His Cys
450 455 460

Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu Cys Pro Thr Gly Phe Ser
465 470 475 480

Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr Cys Glu Pro Asn Pro Cys
485 490 495

Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala Ser Asp Tyr Phe Cys Lys
500 505 510

Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys Ser His Leu Lys Asp His
515 520 525

Cys Arg Thr Thr Pro Cys Glu Val Ile Asp Ser Cys Thr Val Ala Met
530 535 540

Ala Ser Asn Asp Thr Pro Glu Gly Val Arg Tyr Ile Ser Ser Asn Val
545 550 555 560

Cys Gly Pro His Gly Lys Cys Lys Ser Gln Ser Gly Gly Lys Phe Thr
565 570 575

Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr Tyr Cys His Glu Asn Ile
580 585 590

Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn Gly Gly Thr Cys Ile Asp
595 600 605

Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser Asp Gly Trp Glu Gly Ala
610 615 620

Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser Gln Asn Pro Cys His Asn
 625 630 635 640
 Gly Gly Thr Cys Arg Asp Leu Val Asn Asp Phe Tyr Cys Asp Cys Lys
 645 650 655
 Asn Gly Trp Lys Gly Lys Thr Cys His Ser Arg Asp Ser Gln Cys Asp
 660 665 670
 Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys Tyr Asp Glu Gly Asp Ala
 675 680 685
 Phe Lys Cys Met Cys Pro Gly Gly Trp Glu Gly Thr Thr Cys Asn Ile
 690 695 700
 Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro Cys His Asn Gly Gly Thr
 705 710 715 720
 Cys Val Val Asn Gly Glu Ser Phe Thr Cys Val Cys Lys Glu Gly Trp
 725 730 735
 Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn Asp Cys Ser Pro His Pro
 740 745 750
 Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly Asp Asn Trp Tyr Arg Cys
 755 760 765
 Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp Cys Arg Ile Asn Ile Asn
 770 775 780
 Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly Ala Thr Cys Val Asp Glu
 785 790 795 800
 Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro Gly His Ser Gly Ala Lys
 805 810 815
 Cys Gln Glu Val Ser Gly Arg Pro Cys Ile Thr Met Gly Ser Val Ile
 820 825 830
 Pro Asp Gly Ala Lys Trp Asp Asp Asp Cys Asn Thr Cys Gln Cys Leu
 835 840 845
 Asn Gly Arg Ile Ala Cys Ser Lys Val Trp Cys Gly Pro Arg Pro Cys
 850 855 860
 Leu Leu His Lys Gly His Ser Glu Cys Pro Ser Gly Gln Ser Cys Ile
 865 870 875 880
 Pro Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys Thr Gly Val Gly
 885 890 895
 Glu Cys Arg Ser Ser Ser Leu Gln Pro Val Lys Thr Lys Cys Thr Ser
 900 905 910
 Asp Ser Tyr Tyr Gln Asp Asn Cys Ala Asn Ile Thr Phe Thr Phe Asn
 915 920 925

Lys Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile Cys Ser Glu
930 935 940

Leu Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu Tyr Ser Ile
945 950 955 960

Tyr Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu Ile His Val
965 970 975

Ala Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro Ile Lys Glu
980 985 990

Ile Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp Gly Asn Ser
995 1000 1005

Ser Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg Arg Pro
1010 1015 1020

Leu Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser Val
1025 1030 1035

Leu Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp
1040 1045 1050

Cys Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala
1055 1060 1065

Ser Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln
1070 1075 1080

Ile Lys Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile
1085 1090 1095

Lys Asp Tyr Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr
1100 1105 1110

His Asn Ser Glu Val Glu Glu Asp Asp Met Asp Lys His Gln Gln
1115 1120 1125

Lys Ala Arg Phe Ala Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg
1130 1135 1140

Glu Glu Lys Pro Pro Asn Gly Thr Pro Thr Lys His Pro Asn Trp
1145 1150 1155

Thr Asn Lys Gln Asp Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu
1160 1165 1170

Asn Arg Met Glu Tyr Ile Val
1175 1180

<210> 116

<211> 1160

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 116

Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu
 1 5 10 15
 Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30
 Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45
 Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60
 Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80
 Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95
 Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110
 Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125
 Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140
 Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160
 Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175
 Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300

Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
305 310 315 320

Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
325 330 335

Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
340 345 350

Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
355 360 365

Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
370 375 380

His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
385 390 395 400

Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys
405 410 415

Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala
420 425 430

Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp
435 440 445

Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys
450 455 460

Arg Leu Asp Ile Asp Tyr Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala
465 470 475 480

Gln Cys Tyr Asn Arg Ala Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp
485 490 495

Tyr Glu Gly Lys Asn Cys Ser His Leu Lys Asp His Cys Arg Thr Thr
500 505 510

Pro Cys Glu Val Ile Asp Ser Cys Thr Val Ala Met Ala Ser Asn Asp
515 520 525

Thr Pro Glu Gly Val Arg Tyr Ile Ser Ser Asn Val Cys Gly Pro His
530 535 540

Gly Lys Cys Lys Ser Gln Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn
545 550 555 560

Lys Gly Phe Thr Gly Thr Tyr Cys His Glu Asn Ile Asn Asp Cys Glu
565 570 575

Ser Asn Pro Cys Arg Asn Gly Gly Thr Cys Ile Asp Gly Val Asn Ser
580 585 590

Tyr Lys Cys Ile Cys Ser Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr
595 600 605

Asn Ile Asn Asp Cys Ser Gln Asn Pro Cys His Asn Gly Gly Thr Cys

610 615 620
 Arg Asp Leu Val Asn Asp Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys
 625 630 635 640
 Gly Lys Thr Cys His Ser Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys
 645 650 655
 Asn Asn Gly Gly Thr Cys Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met
 660 665 670
 Cys Pro Gly Gly Trp Glu Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser
 675 680 685
 Ser Cys Leu Pro Asn Pro Cys His Asn Gly Gly Thr Cys Val Val Asn
 690 695 700
 Gly Glu Ser Phe Thr Cys Val Cys Lys Glu Gly Trp Glu Gly Pro Ile
 705 710 715 720
 Cys Ala Gln Asn Thr Asn Asp Cys Ser Pro His Pro Cys Tyr Asn Ser
 725 730 735
 Gly Thr Cys Val Asp Gly Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro
 740 745 750
 Gly Phe Ala Gly Pro Asp Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser
 755 760 765
 Ser Pro Cys Ala Phe Gly Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr
 770 775 780
 Arg Cys Val Cys Pro Pro Gly His Ser Gly Ala Lys Cys Gln Glu Val
 785 790 795 800
 Ser Gly Arg Pro Cys Ile Thr Met Gly Ser Val Ile Pro Asp Gly Ala
 805 810 815
 Lys Trp Asp Asp Asp Cys Asn Thr Cys Gln Cys Leu Asn Gly Arg Ile
 820 825 830
 Ala Cys Ser Lys Val Trp Cys Gly Pro Arg Pro Cys Leu Leu His Lys
 835 840 845
 Gly His Ser Glu Cys Pro Ser Gly Gln Ser Cys Ile Pro Ile Leu Asp
 850 855 860
 Asp Gln Cys Phe Val His Pro Cys Thr Gly Val Gly Glu Cys Arg Ser
 865 870 875 880
 Ser Ser Leu Gln Pro Val Lys Thr Lys Cys Thr Ser Asp Ser Tyr Tyr
 885 890 895
 Gln Asp Asn Cys Ala Asn Ile Thr Phe Thr Phe Asn Lys Glu Met Met
 900 905 910
 Ser Pro Gly Leu Thr Thr Glu His Ile Cys Ser Glu Leu Arg Asn Leu
 915 920 925

Asn Ile Leu Lys Asn Val Ser Ala Glu Tyr Ser Ile Tyr Ile Ala Cys
930 935 940

Glu Pro Ser Pro Ser Ala Asn Asn Glu Ile His Val Ala Ile Ser Ala
945 950 955 960

Glu Asp Ile Arg Asp Asp Gly Asn Pro Ile Lys Glu Ile Thr Asp Lys
965 970 975

Ile Ile Asp Leu Val Ser Lys Arg Asp Gly Asn Ser Ser Leu Ile Ala
980 985 990

Ala Val Ala Glu Val Arg Val Gln Arg Arg Pro Leu Lys Asn Arg Thr
995 1000 1005

Asp Phe Leu Val Pro Leu Leu Ser Ser Val Leu Thr Val Ala Trp
1010 1015 1020

Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp Cys Leu Arg Lys Arg
1025 1030 1035

Arg Lys Pro Gly Ser His Thr His Ser Ala Ser Glu Asp Asn Thr
1040 1045 1050

Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile Lys Asn Pro Ile
1055 1060 1065

Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys Asp Tyr Glu Asn
1070 1075 1080

Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His Asn Ser Glu Val
1085 1090 1095

Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys Ala Arg Phe Ala
1100 1105 1110

Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu Glu Lys Pro Pro
1115 1120 1125

Asn Gly Thr Pro Thr Lys His Pro Asn Trp Thr Asn Lys Gln Asp
1130 1135 1140

Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu Asn Arg Met Glu Tyr
1145 1150 1155

Ile Val
1160

<210> 117
<211> 1179
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 117
Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu

1 5 10 15
 Leu Leu Ala Leu Leu Cys Ala Leu Arg Ala Lys Val Cys Gly Ala Ser
 20 25 30
 Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45
 Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60
 Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80
 Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95
 Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110
 Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125
 Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140
 Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160
 Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175
 Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300
 Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
 305 310 315 320

Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
 325 330 335
 Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
 340 345 350
 Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
 355 360 365
 Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
 370 375 380
 His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
 385 390 395 400
 Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys
 405 410 415
 Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala
 420 425 430
 Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp
 435 440 445
 Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys
 450 455 460
 Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala
 465 470 475 480
 Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys
 485 490 495
 Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu
 500 505 510
 Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr
 515 520 525
 Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala
 530 535 540
 Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys
 545 550 555 560
 Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp
 565 570 575
 Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg
 580 585 590
 Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln
 595 600 605
 Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr
 610 615 620

Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn
625 630 635 640

Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser
645 650 655

Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser
660 665 670

Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp
675 680 685

Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser
690 695 700

Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys
705 710 715 720

Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu
725 730 735

Gly Thr Thr Cys Asn Ile Asp Thr Asn Asp Cys Ser Pro His Pro Cys
740 745 750

Tyr Asn Ser Gly Thr Cys Val Asp Gly Asp Asn Trp Tyr Arg Cys Glu
755 760 765

Cys Ala Pro Gly Phe Ala Gly Pro Asp Cys Arg Ile Asn Ile Asn Glu
770 775 780

Cys Gln Ser Ser Pro Cys Ala Phe Gly Ala Thr Cys Val Asp Glu Ile
785 790 795 800

Asn Gly Tyr Arg Cys Val Cys Pro Pro Gly His Ser Gly Ala Lys Cys
805 810 815

Gln Glu Val Ser Gly Arg Pro Cys Ile Thr Met Gly Ser Val Ile Pro
820 825 830

Asp Gly Ala Lys Trp Asp Asp Asp Cys Asn Thr Cys Gln Cys Leu Asn
835 840 845

Gly Arg Ile Ala Cys Ser Lys Val Trp Cys Gly Pro Arg Pro Cys Leu
850 855 860

Leu His Lys Gly His Ser Glu Cys Pro Ser Gly Gln Ser Cys Ile Pro
865 870 875 880

Ile Leu Asp Asp Gln Cys Phe Val His Pro Cys Thr Gly Val Gly Glu
885 890 895

Cys Arg Ser Ser Ser Leu Gln Pro Val Lys Thr Lys Cys Thr Ser Asp
900 905 910

Ser Tyr Tyr Gln Asp Asn Cys Ala Asn Ile Thr Phe Thr Phe Asn Lys
915 920 925

Glu Met Met Ser Pro Gly Leu Thr Thr Glu His Ile Cys Ser Glu Leu
930 935 940

Arg Asn Leu Asn Ile Leu Lys Asn Val Ser Ala Glu Tyr Ser Ile Tyr
945 950 955 960

Ile Ala Cys Glu Pro Ser Pro Ser Ala Asn Asn Glu Ile His Val Ala
965 970 975

Ile Ser Ala Glu Asp Ile Arg Asp Asp Gly Asn Pro Ile Lys Glu Ile
980 985 990

Thr Asp Lys Ile Ile Asp Leu Val Ser Lys Arg Asp Gly Asn Ser Ser
995 1000 1005

Leu Ile Ala Ala Val Ala Glu Val Arg Val Gln Arg Arg Pro Leu
1010 1015 1020

Lys Asn Arg Thr Asp Phe Leu Val Pro Leu Leu Ser Ser Val Leu
1025 1030 1035

Thr Val Ala Trp Ile Cys Cys Leu Val Thr Ala Phe Tyr Trp Cys
1040 1045 1050

Leu Arg Lys Arg Arg Lys Pro Gly Ser His Thr His Ser Ala Ser
1055 1060 1065

Glu Asp Asn Thr Thr Asn Asn Val Arg Glu Gln Leu Asn Gln Ile
1070 1075 1080

Lys Asn Pro Ile Glu Lys His Gly Ala Asn Thr Val Pro Ile Lys
1085 1090 1095

Asp Tyr Glu Asn Lys Asn Ser Lys Met Ser Lys Ile Arg Thr His
1100 1105 1110

Asn Ser Glu Val Glu Glu Asp Asp Met Asp Lys His Gln Gln Lys
1115 1120 1125

Ala Arg Phe Ala Lys Gln Pro Ala Tyr Thr Leu Val Asp Arg Glu
1130 1135 1140

Glu Lys Pro Pro Asn Gly Thr Pro Thr Lys His Pro Asn Trp Thr
1145 1150 1155

Asn Lys Gln Asp Asn Arg Asp Leu Glu Ser Ala Gln Ser Leu Asn
1160 1165 1170

Arg Met Glu Tyr Ile Val
1175

<210> 118

<211> 912

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 118

Met Arg Ser Pro Arg Thr Arg Gly Arg Ser Gly Arg Pro Leu Ser Leu
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 20 25 30
 Gly Gln Phe Glu Leu Glu Ile Leu Ser Met Gln Asn Val Asn Gly Glu
 35 40 45
 Leu Gln Asn Gly Asn Cys Cys Gly Gly Ala Arg Asn Pro Gly Asp Arg
 50 55 60
 Lys Cys Thr Arg Asp Glu Cys Asp Thr Tyr Phe Lys Val Cys Leu Lys
 65 70 75 80
 Glu Tyr Gln Ser Arg Val Thr Ala Gly Gly Pro Cys Ser Phe Gly Ser
 85 90 95
 Gly Ser Thr Pro Val Ile Gly Gly Asn Thr Phe Asn Leu Lys Ala Ser
 100 105 110
 Arg Gly Asn Asp Arg Asn Arg Ile Val Leu Pro Phe Ser Phe Ala Trp
 115 120 125
 Pro Arg Ser Tyr Thr Leu Leu Val Glu Ala Trp Asp Ser Ser Asn Asp
 130 135 140
 Thr Val Gln Pro Asp Ser Ile Ile Glu Lys Ala Ser His Ser Gly Met
 145 150 155 160
 Ile Asn Pro Ser Arg Gln Trp Gln Thr Leu Lys Gln Asn Thr Gly Val
 165 170 175
 Ala His Phe Glu Tyr Gln Ile Arg Val Thr Cys Asp Asp Tyr Tyr Tyr
 180 185 190
 Gly Phe Gly Cys Asn Lys Phe Cys Arg Pro Arg Asp Asp Phe Phe Gly
 195 200 205
 His Tyr Ala Cys Asp Gln Asn Gly Asn Lys Thr Cys Met Glu Gly Trp
 210 215 220
 Met Gly Pro Glu Cys Asn Arg Ala Ile Cys Arg Gln Gly Cys Ser Pro
 225 230 235 240
 Lys His Gly Ser Cys Lys Leu Pro Gly Asp Cys Arg Cys Gln Tyr Gly
 245 250 255
 Trp Gln Gly Leu Tyr Cys Asp Lys Cys Ile Pro His Pro Gly Cys Val
 260 265 270
 His Gly Ile Cys Asn Glu Pro Trp Gln Cys Leu Cys Glu Thr Asn Trp
 275 280 285
 Gly Gly Gln Leu Cys Asp Lys Asp Leu Asn Tyr Cys Gly Thr His Gln
 290 295 300

Pro Cys Leu Asn Gly Gly Thr Cys Ser Asn Thr Gly Pro Asp Lys Tyr
305 310 315 320

Gln Cys Ser Cys Pro Glu Gly Tyr Ser Gly Pro Asn Cys Glu Ile Ala
325 330 335

Glu His Ala Cys Leu Ser Asp Pro Cys His Asn Arg Gly Ser Cys Lys
340 345 350

Glu Thr Ser Leu Gly Phe Glu Cys Glu Cys Ser Pro Gly Trp Thr Gly
355 360 365

Pro Thr Cys Ser Thr Asn Ile Asp Asp Cys Ser Pro Asn Asn Cys Ser
370 375 380

His Gly Gly Thr Cys Gln Asp Leu Val Asn Gly Phe Lys Cys Val Cys
385 390 395 400

Pro Pro Gln Trp Thr Gly Lys Thr Cys Gln Leu Asp Ala Asn Glu Cys
405 410 415

Glu Ala Lys Pro Cys Val Asn Ala Lys Ser Cys Lys Asn Leu Ile Ala
420 425 430

Ser Tyr Tyr Cys Asp Cys Leu Pro Gly Trp Met Gly Gln Asn Cys Asp
435 440 445

Ile Asn Ile Asn Asp Cys Leu Gly Gln Cys Gln Asn Asp Ala Ser Cys
450 455 460

Arg Asp Leu Val Asn Gly Tyr Arg Cys Ile Cys Pro Pro Gly Tyr Ala
465 470 475 480

Gly Asp His Cys Glu Arg Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys
485 490 495

Leu Asn Gly Gly His Cys Gln Asn Glu Ile Asn Arg Phe Gln Cys Leu
500 505 510

Cys Pro Thr Gly Phe Ser Gly Asn Leu Cys Gln Leu Asp Ile Asp Tyr
515 520 525

Cys Glu Pro Asn Pro Cys Gln Asn Gly Ala Gln Cys Tyr Asn Arg Ala
530 535 540

Ser Asp Tyr Phe Cys Lys Cys Pro Glu Asp Tyr Glu Gly Lys Asn Cys
545 550 555 560

Ser His Leu Lys Asp His Cys Arg Thr Thr Pro Cys Glu Val Ile Asp
565 570 575

Ser Cys Thr Val Ala Met Ala Ser Asn Asp Thr Pro Glu Gly Val Arg
580 585 590

Tyr Ile Ser Ser Asn Val Cys Gly Pro His Gly Lys Cys Lys Ser Gln
595 600 605

Ser Gly Gly Lys Phe Thr Cys Asp Cys Asn Lys Gly Phe Thr Gly Thr

610. 615 620
Tyr Cys His Glu Asn Ile Asn Asp Cys Glu Ser Asn Pro Cys Arg Asn
625 630 635 640
Gly Gly Thr Cys Ile Asp Gly Val Asn Ser Tyr Lys Cys Ile Cys Ser
645 650 655
Asp Gly Trp Glu Gly Ala Tyr Cys Glu Thr Asn Ile Asn Asp Cys Ser
660 665 670
Gln Asn Pro Cys His Asn Gly Gly Thr Cys Arg Asp Leu Val Asn Asp
675 680 685
Phe Tyr Cys Asp Cys Lys Asn Gly Trp Lys Gly Lys Thr Cys His Ser
690 695 700
Arg Asp Ser Gln Cys Asp Glu Ala Thr Cys Asn Asn Gly Gly Thr Cys
705 710 715 720
Tyr Asp Glu Gly Asp Ala Phe Lys Cys Met Cys Pro Gly Gly Trp Glu
725 730 735
Gly Thr Thr Cys Asn Ile Ala Arg Asn Ser Ser Cys Leu Pro Asn Pro
740 745 750
Cys His Asn Gly Gly Thr Cys Val Val Asn Gly Glu Ser Phe Thr Cys
755 760 765
Val Cys Lys Glu Gly Trp Glu Gly Pro Ile Cys Ala Gln Asn Thr Asn
770 775 780
Asp Cys Ser Pro His Pro Cys Tyr Asn Ser Gly Thr Cys Val Asp Gly
785 790 795 800
Asp Asn Trp Tyr Arg Cys Glu Cys Ala Pro Gly Phe Ala Gly Pro Asp
805 810 815
Cys Arg Ile Asn Ile Asn Glu Cys Gln Ser Ser Pro Cys Ala Phe Gly
820 825 830
Ala Thr Cys Val Asp Glu Ile Asn Gly Tyr Arg Cys Val Cys Pro Pro
835 840 845
Gly His Ser Gly Ala Lys Cys Gln Glu Gly Leu Val Pro Ser Ile Leu
850 855 860
Pro Ala Pro Gln Arg Ala Gln Arg Val Pro Gln Arg Ala Glu Leu His
865 870 875 880
Pro His Pro Gly Arg Pro Val Leu Arg Pro Pro Leu His Trp Cys Gly
885 890 895
Arg Val Ser Val Phe Gln Ser Pro Ala Gly Glu Asp Lys Val His Leu
900 905 910

<210> 119
<211> 2433

<212> PRT

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 119

Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp
 1 5 10 15

Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly Tyr
 20 25 30

Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn Gly Thr
 35 40 45

Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His
 50 55 60

Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val
 65 70 75 80

Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe
 85 90 95

Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser
 100 105 110

Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg Asp Thr
 115 120 125

Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys Gln Trp
 130 135 140

Thr Asp Ala Cys Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr
 145 150 155 160

Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly
 165 170 175

Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys
 180 185 190

Gln His Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln
 195 200 205

Cys Pro Gln Gly Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro
 210 215 220

Cys Ala Pro Ser Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly
 225 230 235 240

Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Gly Phe Glu Gly Ser Thr
 245 250 255

Cys Glu Arg Asn Ile Asp Asp Cys Pro Asn His Arg Cys Gln Asn Gly
 260 265 270

Gly Val Cys Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro

275 280 285
 Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp Glu Cys Leu Leu
 290 295 300
 Gln Pro Asn Ala Cys Gln Asn Gly Gly Thr Cys Ala Asn Arg Asn Gly
 305 310 315 320
 Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser Gly Asp Asp Cys Ser
 325 330 335
 Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys Thr Pro Gly Ser Thr
 340 345 350
 Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met Cys Pro Glu Gly Lys
 355 360 365
 Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys Ile Ser Asn Pro Cys
 370 375 380
 His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile
 385 390 395 400
 Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val
 405 410 415
 Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys
 420 425 430
 Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr
 435 440 445
 Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro
 450 455 460
 Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys
 465 470 475 480
 Leu Cys Met Pro Gly Phe Thr Gly Pro Val Cys Gln Ile Asp Ile Asp
 485 490 495
 Asp Cys Ser Ser Thr Pro Cys Leu Asn Gly Ala Lys Cys Ile Asp His
 500 505 510
 Pro Asn Gly Tyr Glu Cys Gln Cys Ala Thr Gly Phe Thr Gly Val Leu
 515 520 525
 Cys Glu Glu Asn Ile Asp Asn Cys Asp Pro Asp Pro Cys His His Gly
 530 535 540
 Gln Cys Gln Asp Gly Ile Asp Ser Tyr Thr Cys Ile Cys Asn Pro Gly
 545 550 555 560
 Tyr Met Gly Ala Ile Cys Ser Asp Gln Ile Asp Glu Cys Tyr Ser Ser
 565 570 575
 Pro Cys Leu Asn Asp Gly Arg Cys Ile Asp Leu Val Asn Gly Tyr Gln
 580 585 590

Cys Asn Cys Gln Pro Gly Thr Ser Gly Val Asn Cys Glu Ile Asn Phe
 595 600 605
 Asp Asp Cys Ala Ser Asn Pro Cys Ile His Gly Ile Cys Met Asp Gly
 610 615 620
 Ile Asn Arg Tyr Ser Cys Val Cys Ser Pro Gly Phe Thr Gly Gln Arg
 625 630 635 640
 Cys Asn Ile Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys Arg Lys Gly
 645 650 655
 Ala Thr Cys Ile Asn Gly Val Asn Gly Phe Arg Cys Ile Cys Pro Glu
 660 665 670
 Gly Pro His His Pro Ser Cys Tyr Ser Gln Val Asn Glu Cys Leu Ser
 675 680 685
 Asn Pro Cys Ile His Gly Asn Cys Thr Gly Gly Leu Ser Gly Tyr Lys
 690 695 700
 Cys Leu Cys Asp Ala Gly Trp Val Gly Ile Asn Cys Glu Val Asp Lys
 705 710 715 720
 Asn Glu Cys Leu Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Asp Asn
 725 730 735
 Leu Val Asn Gly Tyr Arg Cys Thr Cys Lys Lys Gly Phe Lys Gly Tyr
 740 745 750
 Asn Cys Gln Val Asn Ile Asp Glu Cys Ala Ser Asn Pro Cys Leu Asn
 755 760 765
 Gln Gly Thr Cys Phe Asp Asp Ile Ser Gly Tyr Thr Cys His Cys Val
 770 775 780
 Leu Pro Tyr Thr Gly Lys Asn Cys Gln Thr Val Leu Ala Pro Cys Ser
 785 790 795 800
 Pro Asn Pro Cys Glu Asn Ala Ala Val Cys Lys Glu Ser Pro Asn Phe
 805 810 815
 Glu Ser Tyr Thr Cys Leu Cys Ala Pro Gly Trp Gln Gly Gln Arg Cys
 820 825 830
 Thr Ile Asp Ile Asp Glu Cys Ile Ser Lys Pro Cys Met Asn His Gly
 835 840 845
 Leu Cys His Asn Thr Gln Gly Ser Tyr Met Cys Glu Cys Pro Pro Gly
 850 855 860
 Phe Ser Gly Met Asp Cys Glu Glu Asp Ile Asp Asp Cys Leu Ala Asn
 865 870 875 880
 Pro Cys Gln Asn Gly Gly Ser Cys Met Asp Gly Val Asn Thr Phe Ser
 885 890 895

Cys Leu Cys Leu Pro Gly Phe Thr Gly Asp Lys Cys Gln Thr Asp Met
 900 905 910
 Asn Glu Cys Leu Ser Glu Pro Cys Lys Asn Gly Gly Thr Cys Ser Asp
 915 920 925
 Tyr Val Asn Ser Tyr Thr Cys Lys Cys Gln Ala Gly Phe Asp Gly Val
 930 935 940
 His Cys Glu Asn Asn Ile Asn Glu Cys Thr Glu Ser Ser Cys Phe Asn
 945 950 955 960
 Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Ser Cys Leu Cys Pro
 965 970 975
 Val Gly Phe Thr Gly Ser Phe Cys Leu His Glu Ile Asn Glu Cys Ser
 980 985 990
 Ser His Pro Cys Leu Asn Glu Gly Thr Cys Val Asp Gly Leu Gly Thr
 995 1000 1005
 Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr Gly Lys Asn Cys Gln
 1010 1015 1020
 Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys Lys Asn Lys Gly
 1025 1030 1035
 Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu Cys Pro Ser
 1040 1045 1050
 Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser Cys Asp
 1055 1060 1065
 Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys Gln
 1070 1075 1080
 His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys Gln
 1085 1090 1095
 Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu Asp
 1100 1105 1110
 Glu Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser Asp
 1115 1120 1125
 Phe Ile Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln Gly
 1130 1135 1140
 Val Asn Cys Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro Cys
 1145 1150 1155
 Gln Asn Gly Gly Thr Cys Ile Asp Leu Val Asn His Phe Lys Cys
 1160 1165 1170
 Ser Cys Pro Pro Gly Thr Arg Gly Leu Leu Cys Glu Glu Asn Ile
 1175 1180 1185

Asp Asp Cys Ala Arg Gly Pro His Cys Leu Asn Gly Gly Gln Cys
 1190 1195 1200
 Met Asp Arg Ile Gly Gly Tyr Ser Cys Arg Cys Leu Pro Gly Phe
 1205 1210 1215
 Ala Gly Glu Arg Cys Glu Gly Asp Ile Asn Glu Cys Leu Ser Asn
 1220 1225 1230
 Pro Cys Ser Ser Glu Gly Ser Leu Asp Cys Ile Gln Leu Thr Asn
 1235 1240 1245
 Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe Thr Gly Arg His Cys
 1250 1255 1260
 Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro Cys Leu Asn Gly
 1265 1270 1275
 Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly Phe Ile Cys
 1280 1285 1290
 Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser Ser Cys
 1295 1300 1305
 Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr Ala
 1310 1315 1320
 Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu Ser
 1325 1330 1335
 Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His Pro
 1340 1345 1350
 Gln Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro Phe
 1355 1360 1365
 Ser Gly Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr Pro
 1370 1375 1380
 Pro Ala Thr Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg Asp
 1385 1390 1395
 Gly Val Cys Asp Glu Ala Cys Asn Ser His Ala Cys Gln Trp Asp
 1400 1405 1410
 Gly Gly Asp Cys Ser Leu Thr Met Glu Asn Pro Trp Ala Asn Cys
 1415 1420 1425
 Ser Ser Pro Leu Pro Cys Trp Asp Tyr Ile Asn Asn Gln Cys Asp
 1430 1435 1440
 Glu Leu Cys Asn Thr Val Glu Cys Leu Phe Asp Asn Phe Glu Cys
 1445 1450 1455
 Gln Gly Asn Ser Lys Thr Cys Lys Tyr Asp Lys Tyr Cys Ala Asp
 1460 1465 1470
 His Phe Lys Asp Asn His Cys Asn Gln Gly Cys Asn Ser Glu Glu

1475	1480	1485
Cys Gly Trp Asp Gly Leu Asp	Cys Ala Ala Asp Gln	Pro Glu Asn
1490	1495	1500
Leu Ala Glu Gly Thr Leu Val	Ile Val Val Leu Met	Pro Pro Glu
1505	1510	1515
Gln Leu Leu Gln Asp Ala Arg	Ser Phe Leu Arg Ala	Leu Gly Thr
1520	1525	1530
Leu Leu His Thr Asn Leu Arg	Ile Lys Arg Asp Ser	Gln Gly Glu
1535	1540	1545
Leu Met Val Tyr Pro Tyr Tyr	Gly Glu Lys Ser Ala	Ala Met Lys
1550	1555	1560
Lys Gln Arg Met Thr Arg Arg	Ser Leu Pro Gly Glu	Gln Glu Gln
1565	1570	1575
Glu Val Ala Gly Ser Lys Val	Phe Leu Glu Ile Asp	Asn Arg Gln
1580	1585	1590
Cys Val Gln Asp Ser Asp His	Cys Phe Lys Asn Thr	Asp Ala Ala
1595	1600	1605
Ala Ala Leu Leu Ala Ser His	Ala Ile Gln Gly Thr	Leu Ser Tyr
1610	1615	1620
Pro Leu Val Ser Val Val Ser	Glu Ser Leu Thr Pro	Glu Arg Thr
1625	1630	1635
Gln Leu Leu Tyr Leu Leu Ala	Val Ala Val Val Ile	Ile Leu Phe
1640	1645	1650
Ile Ile Leu Leu Gly Val Ile	Met Ala Lys Arg Lys	Arg Lys His
1655	1660	1665
Gly Ser Leu Trp Leu Pro Glu	Gly Phe Thr Leu Arg	Arg Asp Ala
1670	1675	1680
Ser Asn His Lys Arg Arg Glu	Pro Val Gly Gln Asp	Ala Val Gly
1685	1690	1695
Leu Lys Asn Leu Ser Val Gln	Val Ser Glu Ala Asn	Leu Ile Gly
1700	1705	1710
Thr Gly Thr Ser Glu His Trp	Val Asp Asp Glu Gly	Pro Gln Pro
1715	1720	1725
Lys Lys Val Lys Ala Glu Asp	Glu Ala Leu Leu Ser	Glu Glu Asp
1730	1735	1740
Asp Pro Ile Asp Arg Arg Pro	Trp Thr Gln Gln His	Leu Glu Ala
1745	1750	1755
Ala Asp Ile Arg Arg Thr Pro	Ser Leu Ala Leu Thr	Pro Pro Gln
1760	1765	1770

Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro
 1775 1780 1785
 Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser
 1790 1795 1800
 Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala
 1805 1810 1815
 Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala
 1820 1825 1830
 Gln Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala Arg
 1835 1840 1845
 Tyr Ser Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly Ala
 1850 1855 1860
 Asp Ala Asn Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His Ala
 1865 1870 1875
 Ala Val Ala Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile Arg
 1880 1885 1890
 Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn Asp Gly Thr Thr
 1895 1900 1905
 Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Val Ala
 1910 1915 1920
 Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp Asp His
 1925 1930 1935
 Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val Glu
 1940 1945 1950
 Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met Gln
 1955 1960 1965
 Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly
 1970 1975 1980
 Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg
 1985 1990 1995
 Asp Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg
 2000 2005 2010
 Asp Arg Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn
 2015 2020 2025
 Val Thr Pro Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser
 2030 2035 2040
 Pro Val Ile Cys Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His
 2045 2050 2055

Thr Pro Met Gly Lys Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr
 2060 2065 2070
 Met Pro Thr Ser Leu Pro Asn Leu Ala Lys Glu Ala Lys Asp Ala
 2075 2080 2085
 Lys Gly Ser Arg Arg Lys Lys Ser Leu Ser Glu Lys Val Gln Leu
 2090 2095 2100
 Ser Glu Ser Ser Val Thr Leu Ser Pro Val Asp Ser Leu Glu Ser
 2105 2110 2115
 Pro His Thr Tyr Val Ser Asp Thr Thr Ser Ser Pro Met Ile Thr
 2120 2125 2130
 Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn Pro Met Leu Ala Thr
 2135 2140 2145
 Ala Ala Pro Pro Ala Pro Val His Ala Gln His Ala Leu Ser Phe
 2150 2155 2160
 Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly Ala Ser Thr
 2165 2170 2175
 Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His Ile Val
 2180 2185 2190
 Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His Pro
 2195 2200 2205
 Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu
 2210 2215 2220
 Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu
 2225 2230 2235
 Gly Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly
 2240 2245 2250
 Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr
 2255 2260 2265
 Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala
 2270 2275 2280
 Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu
 2285 2290 2295
 Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser Val
 2300 2305 2310
 Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val Ala
 2315 2320 2325
 Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val Gly
 2330 2335 2340

Lys Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser Asn
2345 2350 2355

Ala Ala Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly Glu
2360 2365 2370

His Pro Tyr Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp Ser
2375 2380 2385

Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser Asp Val Thr Thr
2390 2395 2400

Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg Gly Pro Gly
2405 2410 2415

Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val Tyr Ala
2420 2425 2430

<210> 120

<211> 2434

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 120

Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp
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Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly Tyr
20 25 30

Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn Gly Thr
35 40 45

Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His
50 55 60

Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val
65 70 75 80

Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe
85 90 95

Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser
100 105 110

Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg Asp Thr
115 120 125

Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys Gln Trp
130 135 140

Thr Asp Ala Cys Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr
145 150 155 160

Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly
165 170 175

Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys
 180 185 190

Gln His Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln
 195 200 205

Cys Pro Gln Gly Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro
 210 215 220

Cys Ala Pro Ser Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly
 225 230 235 240

Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Gly Phe Glu Gly Ser Thr
 245 250 255

Cys Glu Arg Asn Ile Asp Asp Cys Pro Asn His Arg Cys Gln Asn Gly
 260 265 270

Gly Val Cys Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro
 275 280 285

Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp Glu Cys Leu Leu
 290 295 300

Gln Pro Asp Ala Cys Gln Asn Gly Gly Thr Cys Ala Asn Arg Asn Gly
 305 310 315 320

Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser Gly Asp Asp Cys Ser
 325 330 335

Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys Thr Pro Gly Ser Thr
 340 345 350

Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met Cys Pro Glu Gly Lys
 355 360 365

Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys Ile Ser Asn Pro Cys
 370 375 380

His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile
 385 390 395 400

Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val
 405 410 415

Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys
 420 425 430

Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr
 435 440 445

Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro
 450 455 460

Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys
 465 470 475 480

Leu Cys Met Pro Gly Phe Lys Gly Val His Cys Glu Leu Glu Ile Asn
485 490 495

Glu Cys Gln Ser Asn Pro Cys Val Asn Asn Gly Gln Cys Val Asp Lys
500 505 510

Val Asn Arg Phe Gln Cys Leu Cys Pro Pro Gly Phe Thr Gly Pro Val
515 520 525

Cys Gln Ile Asp Ile Asp Asp Cys Ser Ser Thr Pro Cys Leu Asn Gly
530 535 540

Ala Lys Cys Ile Asp His Pro Asn Gly Tyr Glu Cys Gln Cys Ala Thr
545 550 555 560

Gly Phe Thr Gly Val Leu Cys Glu Glu Asn Ile Asp Asn Cys Asp Pro
565 570 575

Asp Pro Cys His His Gly Gln Cys Gln Asp Gly Ile Asp Ser Tyr Thr
580 585 590

Cys Ile Cys Asn Pro Gly Tyr Met Gly Ala Ile Cys Ser Asp Gln Ile
595 600 605

Asp Glu Cys Tyr Ser Ser Pro Cys Leu Asn Asp Gly Arg Cys Ile Asp
610 615 620

Leu Val Asn Gly Tyr Gln Cys Asn Cys Gln Pro Gly Thr Ser Gly Gln
625 630 635 640

Arg Cys Asn Ile Asp Ile Asp Glu Cys Ala Ser Asn Pro Cys Arg Lys
645 650 655

Gly Ala Thr Cys Ile Asn Gly Val Asn Gly Phe Arg Cys Ile Cys Pro
660 665 670

Glu Gly Pro His His Pro Ser Cys Tyr Ser Gln Val Asn Glu Cys Leu
675 680 685

Ser Asn Pro Cys Ile His Gly Asn Cys Thr Gly Gly Leu Ser Gly Tyr
690 695 700

Lys Cys Leu Cys Asp Ala Gly Trp Val Gly Ile Asn Cys Glu Val Asp
705 710 715 720

Lys Asn Glu Cys Leu Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Asp
725 730 735

Asn Leu Val Asn Gly Tyr Arg Cys Thr Cys Lys Lys Gly Phe Lys Gly
740 745 750

Tyr Asn Cys Gln Val Asn Ile Asp Glu Cys Ala Ser Asn Pro Cys Leu
755 760 765

Asn Gln Gly Thr Cys Phe Asp Asp Ile Ser Gly Tyr Thr Cys His Cys
770 775 780

Val Leu Pro Tyr Thr Gly Lys Asn Cys Gln Thr Val Leu Ala Pro Cys

785 790 795 800
 Ser Pro Asn Pro Cys Glu Asn Ala Ala Val Cys Lys Glu Ser Pro Asn
 805 810 815
 Phe Glu Ser Tyr Thr Cys Leu Cys Ala Pro Gly Trp Gln Gly Gln Arg
 820 825 830
 Cys Thr Ile Asp Ile Asp Glu Cys Ile Ser Lys Pro Cys Met Asn His
 835 840 845
 Gly Leu Cys His Asn Thr Gln Gly Ser Tyr Met Cys Glu Cys Pro Pro
 850 855 860
 Gly Phe Ser Gly Met Asp Cys Glu Glu Asp Ile Asp Asp Cys Leu Ala
 865 870 875 880
 Asn Pro Cys Gln Asn Gly Gly Ser Cys Met Asp Gly Val Asn Thr Phe
 885 890 895
 Ser Cys Leu Cys Leu Pro Gly Phe Thr Gly Asp Lys Cys Gln Thr Asp
 900 905 910
 Met Asn Glu Cys Leu Ser Glu Pro Cys Lys Asn Gly Gly Thr Cys Ser
 915 920 925
 Asp Tyr Val Asn Ser Tyr Thr Cys Lys Cys Gln Ala Gly Phe Asp Gly
 930 935 940
 Val His Cys Glu Asn Asn Ile Asn Glu Cys Thr Glu Ser Ser Cys Phe
 945 950 955 960
 Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Ser Cys Leu Cys
 965 970 975
 Pro Val Gly Phe Thr Gly Ser Phe Cys Leu His Glu Ile Asn Glu Cys
 980 985 990
 Ser Ser His Pro Cys Leu Asn Glu Gly Thr Cys Val Asp Gly Leu Gly
 995 1000 1005
 Thr Tyr Arg Cys Ser Cys Pro Leu Gly Tyr Thr Gly Lys Asn Cys
 1010 1015 1020
 Gln Thr Leu Val Asn Leu Cys Ser Arg Ser Pro Cys Lys Asn Lys
 1025 1030 1035
 Gly Thr Cys Val Gln Lys Lys Ala Glu Ser Gln Cys Leu Cys Pro
 1040 1045 1050
 Ser Gly Trp Ala Gly Ala Tyr Cys Asp Val Pro Asn Val Ser Cys
 1055 1060 1065
 Asp Ile Ala Ala Ser Arg Arg Gly Val Leu Val Glu His Leu Cys
 1070 1075 1080
 Gln His Ser Gly Val Cys Ile Asn Ala Gly Asn Thr His Tyr Cys
 1085 1090 1095

Gln Cys Pro Leu Gly Tyr Thr Gly Ser Tyr Cys Glu Glu Gln Leu
 1100 1105 1110
 Asp Glu Cys Ala Ser Asn Pro Cys Gln His Gly Ala Thr Cys Ser
 1115 1120 1125
 Asp Phe Ile Gly Gly Tyr Arg Cys Glu Cys Val Pro Gly Tyr Gln
 1130 1135 1140
 Gly Val Asn Cys Glu Tyr Glu Val Asp Glu Cys Gln Asn Gln Pro
 1145 1150 1155
 Cys Gln Asn Gly Gly Thr Cys Ile Asp Leu Val Asn His Phe Lys
 1160 1165 1170
 Cys Ser Cys Pro Pro Gly Thr Arg Gly Leu Leu Cys Glu Glu Asn
 1175 1180 1185
 Ile Asp Asp Cys Ala Arg Gly Pro His Cys Leu Asn Gly Gly Gln
 1190 1195 1200
 Cys Met Asp Arg Ile Gly Gly Tyr Ser Cys Arg Cys Leu Pro Gly
 1205 1210 1215
 Phe Ala Gly Glu Arg Cys Glu Gly Asp Ile Asn Glu Cys Leu Ser
 1220 1225 1230
 Asn Pro Cys Ser Ser Glu Gly Ser Leu Asp Cys Ile Gln Leu Thr
 1235 1240 1245
 Asn Asp Tyr Leu Cys Val Cys Arg Ser Ala Phe Thr Gly Arg His
 1250 1255 1260
 Cys Glu Thr Phe Val Asp Val Cys Pro Gln Met Pro Cys Leu Asn
 1265 1270 1275
 Gly Gly Thr Cys Ala Val Ala Ser Asn Met Pro Asp Gly Phe Ile
 1280 1285 1290
 Cys Arg Cys Pro Pro Gly Phe Ser Gly Ala Arg Cys Gln Ser Ser
 1295 1300 1305
 Cys Gly Gln Val Lys Cys Arg Lys Gly Glu Gln Cys Val His Thr
 1310 1315 1320
 Ala Ser Gly Pro Arg Cys Phe Cys Pro Ser Pro Arg Asp Cys Glu
 1325 1330 1335
 Ser Gly Cys Ala Ser Ser Pro Cys Gln His Gly Gly Ser Cys His
 1340 1345 1350
 Pro Gln Arg Gln Pro Pro Tyr Tyr Ser Cys Gln Cys Ala Pro Pro
 1355 1360 1365
 Phe Ser Gly Ser Arg Cys Glu Leu Tyr Thr Ala Pro Pro Ser Thr
 1370 1375 1380

Pro Pro Ala Thr Cys Leu Ser Gln Tyr Cys Ala Asp Lys Ala Arg
 1385 1390 1395
 Asp Gly Val Cys Asp Glu Ala Cys Asn Ser His Ala Cys Gln Trp
 1400 1405 1410
 Asp Gly Gly Asp Cys Ser Leu Thr Met Glu Asn Pro Trp Ala Asn
 1415 1420 1425
 Cys Ser Ser Pro Leu Pro Cys Trp Asp Tyr Ile Asn Asn Gln Cys
 1430 1435 1440
 Asp Glu Leu Cys Asn Thr Val Glu Cys Leu Phe Asp Asn Phe Glu
 1445 1450 1455
 Cys Gln Gly Asn Ser Lys Thr Cys Lys Tyr Asp Lys Tyr Cys Ala
 1460 1465 1470
 Asp His Phe Lys Asp Asn His Cys Asn Gln Gly Cys Asn Ser Glu
 1475 1480 1485
 Glu Cys Gly Trp Asp Gly Leu Asp Cys Ala Ala Asp Gln Pro Glu
 1490 1495 1500
 Asn Leu Ala Glu Gly Thr Leu Val Ile Val Val Leu Met Pro Pro
 1505 1510 1515
 Glu Gln Leu Leu Gln Asp Ala Arg Ser Phe Leu Arg Ala Leu Gly
 1520 1525 1530
 Thr Leu Leu His Thr Asn Leu Arg Ile Lys Arg Asp Ser Gln Gly
 1535 1540 1545
 Glu Leu Met Val Tyr Pro Tyr Tyr Gly Glu Lys Ser Ala Ala Met
 1550 1555 1560
 Lys Lys Gln Arg Met Thr Arg Arg Ser Leu Pro Gly Glu Gln Glu
 1565 1570 1575
 Gln Glu Val Ala Gly Ser Lys Val Phe Leu Glu Ile Asp Asn Arg
 1580 1585 1590
 Gln Cys Val Gln Asp Ser Asp His Cys Phe Lys Asn Thr Asp Ala
 1595 1600 1605
 Ala Ala Ala Leu Leu Ala Ser His Ala Ile Gln Gly Thr Leu Ser
 1610 1615 1620
 Tyr Pro Leu Val Ser Val Val Ser Glu Ser Leu Thr Pro Glu Arg
 1625 1630 1635
 Thr Gln Leu Leu Tyr Leu Leu Ala Val Ala Val Val Ile Ile Leu
 1640 1645 1650
 Phe Ile Ile Leu Leu Gly Val Ile Met Ala Lys Arg Lys Arg Lys
 1655 1660 1665

His Gly Ser Leu Trp Leu Pro Glu Gly Phe Thr Leu Arg Arg Asp
 1670 1675 1680
 Ala Ser Asn His Lys Arg Arg Glu Pro Val Gly Gln Asp Ala Val
 1685 1690 1695
 Gly Leu Lys Asn Leu Ser Val Gln Val Ser Glu Ala Asn Leu Ile
 1700 1705 1710
 Gly Thr Gly Thr Ser Glu His Trp Val Asp Asp Glu Gly Pro Gln
 1715 1720 1725
 Pro Lys Lys Val Lys Ala Glu Asp Glu Ala Leu Leu Ser Glu Glu
 1730 1735 1740
 Asp Asp Pro Ile Asp Arg Arg Pro Trp Thr Gln Gln His Leu Glu
 1745 1750 1755
 Ala Ala Asp Ile Arg Arg Thr Pro Ser Leu Ala Leu Thr Pro Pro
 1760 1765 1770
 Gln Ala Glu Gln Glu Val Asp Val Leu Asp Val Asn Val Arg Gly
 1775 1780 1785
 Pro Asp Gly Cys Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly
 1790 1795 1800
 Ser Ser Asp Leu Ser Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser
 1805 1810 1815
 Ala Asn Ile Ile Thr Asp Leu Val Tyr Gln Gly Ala Ser Leu Gln
 1820 1825 1830
 Ala Gln Thr Asp Arg Thr Gly Glu Met Ala Leu His Leu Ala Ala
 1835 1840 1845
 Arg Tyr Ser Arg Ala Asp Ala Ala Lys Arg Leu Leu Asp Ala Gly
 1850 1855 1860
 Ala Asp Ala Asn Ala Gln Asp Asn Met Gly Arg Cys Pro Leu His
 1865 1870 1875
 Ala Ala Val Ala Ala Asp Ala Gln Gly Val Phe Gln Ile Leu Ile
 1880 1885 1890
 Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met Asn Asp Gly Thr
 1895 1900 1905
 Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu Gly Met Val
 1910 1915 1920
 Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val Asp Asp
 1925 1930 1935
 His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn Val
 1940 1945 1950
 Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met

1955	1960	1965
Gln Asp Asn Lys Glu Glu Thr 1970	Pro Leu Phe Leu Ala 1975	Ala Arg Glu 1980
Gly Ser Tyr Glu Ala Ala Lys 1985	Ile Leu Leu Asp 1990	His Phe Ala Asn 1995
Arg Asp Ile Thr Asp His Met 2000	Asp Arg Leu Pro Arg 2005	Asp Val Ala 2010
Arg Asp Arg Met His His Asp 2015	Ile Val Arg Leu Leu 2020	Asp Glu Tyr 2025
Asn Val Thr Pro Ser Pro Pro 2030	Gly Thr Val Leu Thr 2035	Ser Ala Leu 2040
Ser Pro Val Ile Cys Gly Pro 2045	Asn Arg Ser Phe Leu 2050	Ser Leu Lys 2055
His Thr Pro Met Gly Lys Lys 2060	Ser Arg Arg Pro Ser 2065	Ala Lys Ser 2070
Thr Met Pro Thr Ser Leu Pro 2075	Asn Leu Ala Lys Glu 2080	Ala Lys Asp 2085
Ala Lys Gly Ser Arg Arg Lys 2090	Lys Ser Leu Ser Glu 2095	Lys Val Gln 2100
Leu Ser Glu Ser Ser Val Thr 2105	Leu Ser Pro Val Asp 2110	Ser Leu Glu 2115
Ser Pro His Thr Tyr Val Ser 2120	Asp Thr Thr Ser Ser 2125	Pro Met Ile 2130
Thr Ser Pro Gly Ile Leu Gln 2135	Ala Ser Pro Asn Pro 2140	Met Leu Ala 2145
Thr Ala Ala Pro Pro Ala Pro 2150	Val His Ala Gln His 2155	Ala Leu Ser 2160
Phe Ser Asn Leu His Glu Met 2165	Gln Pro Leu Ala His 2170	Gly Ala Ser 2175
Thr Val Leu Pro Ser Val Ser 2180	Gln Leu Leu Ser His 2185	His His Ile 2190
Val Ser Pro Gly Ser Gly Ser 2195	Ala Gly Ser Leu Ser 2200	Arg Leu His 2205
Pro Val Pro Val Pro Ala Asp 2210	Trp Met Asn Arg Met 2215	Glu Val Asn 2220
Glu Thr Gln Tyr Asn Glu Met 2225	Phe Gly Met Val Leu 2230	Ala Pro Ala 2235
Glu Gly Thr His Pro Gly Ile 2240	Ala Pro Gln Ser Arg 2245	Pro Pro Glu 2250

Gly Lys His Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val
2255 2260 2265

Thr Phe Gln Leu Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly
2270 2275 2280

Ala Pro Gln Pro Gln Ser Thr Cys Pro Pro Ala Val Ala Gly Pro
2285 2290 2295

Leu Pro Thr Met Tyr Gln Ile Pro Glu Met Ala Arg Leu Pro Ser
2300 2305 2310

Val Ala Phe Pro Thr Ala Met Met Pro Gln Gln Asp Gly Gln Val
2315 2320 2325

Ala Gln Thr Ile Leu Pro Ala Tyr His Pro Phe Pro Ala Ser Val
2330 2335 2340

Gly Lys Tyr Pro Thr Pro Pro Ser Gln His Ser Tyr Ala Ser Ser
2345 2350 2355

Asn Ala Ala Glu Arg Thr Pro Ser His Ser Gly His Leu Gln Gly
2360 2365 2370

Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser Pro Asp Gln Trp
2375 2380 2385

Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser Asp Val Thr
2390 2395 2400

Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg Gly Pro
2405 2410 2415

Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val Tyr
2420 2425 2430

Ala

<210> 121

<211> 208

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 121

Met Gly Pro Gly Ala Arg Gly Arg Arg Arg Arg Arg Pro Met Ser
1 5 10 15

Pro Pro Pro Pro Pro Pro Val Arg Ala Leu Pro Leu Leu Leu
20 25 30

Leu Ala Gly Pro Gly Ala Ala Gly Ala Arg Leu Ala Gly Trp Val Ser
35 40 45

Gly Val Ser Trp Arg Thr Pro Val Thr Gln Ala Pro Val Leu Ala Val

50 55 60

Val Ser Ala Arg Val Gln Trp Trp Leu Ala Pro Pro Asp Ser His Ala
65 70 75 80

Gly Ala Pro Val Ala Ser Glu Ala Leu Thr Ala Pro Cys Gln Ile Pro
85 90 95

Ala Ser Ala Ala Leu Val Pro Thr Val Pro Ala Ala Gln Trp Gly Pro
100 105 110

Met Asp Ala Ser Ser Ala Pro Ala His Leu Ala Thr Arg Ala Ala Ala
115 120 125

Ala Glu Ala Thr Trp Met Ser Ala Gly Trp Val Ser Pro Ala Ala Met
130 135 140

Val Ala Pro Ala Ser Thr His Leu Ala Pro Ser Ala Ala Ser Val Gln
145 150 155 160

Leu Ala Thr Gln Gly His Tyr Val Arg Thr Pro Arg Cys Pro Val His
165 170 175

Pro His His Ala Val Thr Gly Ala Pro Ala Gly Arg Val Ala Thr Ser
180 185 190

Leu Thr Thr Val Pro Val Phe Leu Gly Leu Arg Val Arg Ile Val Lys
195 200 205

<210> 122
<211> 1938
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 122

Met Gln Pro Pro Ser Leu Leu Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Cys Val Ser Val Val Arg Pro Arg Gly Leu Leu Cys Gly Ser Phe Pro
20 25 30

Glu Pro Cys Ala Asn Gly Gly Thr Cys Leu Ser Leu Ser Leu Gly Gln
35 40 45

Gly Thr Cys Gln Cys Ala Pro Gly Phe Leu Gly Glu Thr Cys Gln Phe
50 55 60

Pro Asp Pro Cys Gln Asn Ala Gln Leu Cys Gln Asn Gly Gly Ser Cys
65 70 75 80

Gln Ala Leu Leu Pro Ala Pro Leu Gly Leu Pro Ser Ser Pro Ser Pro
85 90 95

Leu Thr Pro Ser Phe Leu Cys Thr Cys Leu Pro Gly Phe Thr Gly Glu
100 105 110

Arg Cys Gln Ala Lys Leu Glu Asp Pro Cys Pro Pro Ser Phe Cys Ser
 115 120 125
 Lys Arg Gly Arg Cys His Ile Gln Ala Ser Gly Arg Pro Gln Cys Ser
 130 135 140
 Cys Met Pro Gly Trp Thr Gly Glu Gln Cys Gln Leu Arg Asp Phe Cys
 145 150 155 160
 Ser Ala Asn Pro Cys Val Asn Gly Gly Val Cys Leu Ala Thr Tyr Pro
 165 170 175
 Gln Ile Gln Cys His Cys Pro Pro Gly Phe Glu Gly His Ala Cys Glu
 180 185 190
 Arg Asp Val Asn Glu Cys Phe Gln Asp Pro Gly Pro Cys Pro Lys Gly
 195 200 205
 Thr Ser Cys His Asn Thr Leu Gly Ser Phe Gln Cys Leu Cys Pro Val
 210 215 220
 Gly Gln Glu Gly Pro Arg Cys Glu Leu Arg Ala Gly Pro Cys Pro Pro
 225 230 235 240
 Arg Gly Cys Ser Asn Gly Gly Thr Cys Gln Leu Met Pro Glu Lys Asp
 245 250 255
 Ser Thr Phe His Leu Cys Leu Cys Pro Pro Gly Phe Ile Gly Pro Asp
 260 265 270
 Cys Glu Val Asn Pro Asp Asn Cys Val Ser His Gln Cys Gln Asn Gly
 275 280 285
 Gly Thr Cys Gln Asp Gly Leu Asp Thr Tyr Thr Cys Leu Cys Pro Glu
 290 295 300
 Thr Trp Thr Gly Trp Asp Cys Ser Glu Asp Val Asp Glu Cys Glu Thr
 305 310 315 320
 Gln Gly Pro Pro His Cys Arg Asn Gly Gly Thr Cys Gln Asn Ser Ala
 325 330 335
 Gly Ser Phe His Cys Val Cys Val Ser Gly Trp Gly Gly Thr Ser Cys
 340 345 350
 Glu Glu Asn Leu Asp Asp Cys Ile Ala Ala Thr Cys Ala Pro Gly Ser
 355 360 365
 Thr Cys Ile Asp Arg Val Gly Ser Phe Ser Cys Leu Cys Pro Pro Gly
 370 375 380
 Arg Thr Gly Leu Leu Cys His Leu Glu Asp Met Cys Leu Ser Gln Pro
 385 390 395 400
 Cys His Gly Asp Ala Gln Cys Ser Thr Asn Pro Leu Thr Gly Ser Thr
 405 410 415
 Leu Cys Leu Cys Gln Pro Gly Tyr Ser Gly Pro Thr Cys His Gln Asp

420 425 430
 Leu Asp Glu Cys Leu Met Gly Leu Glu Gly Gln Leu Cys Glu Val Glu
 435 440 445
 Thr Asn Glu Cys Ala Ser Ala Pro Cys Leu Asn His Ala Asp Cys His
 450 455 460
 Asp Leu Leu Asn Gly Phe Gln Cys Ile Cys Leu Pro Gly Phe Ser Gly
 465 470 475 480
 Thr Arg Cys Glu Glu Asp Ile Asp Glu Cys Arg Ser Ser Pro Cys Ala
 485 490 495
 Asn Gly Gly Gln Cys Gln Asp Gln Pro Gly Ala Phe His Cys Lys Cys
 500 505 510
 Leu Pro Gly Phe Glu Gly Pro Arg Cys Gln Thr Glu Val Asp Glu Cys
 515 520 525
 Leu Ser Asp Pro Cys Pro Val Gly Ala Ser Cys Leu Asp Leu Pro Gly
 530 535 540
 Ala Phe Phe Cys Leu Cys Pro Ser Gly Phe Thr Gly Gln Leu Cys Glu
 545 550 555 560
 Val Pro Leu Cys Ala Pro Asn Leu Cys Gln Pro Lys Gln Ile Cys Lys
 565 570 575
 Asp Gln Lys Asp Lys Ala Asn Cys Leu Cys Pro Asp Gly Ser Pro Gly
 580 585 590
 Cys Ala Pro Pro Glu Asp Asn Cys Thr Cys His His Gly His Cys Gln
 595 600 605
 Arg Ser Ser Cys Val Cys Asp Val Gly Trp Thr Gly Pro Glu Cys Glu
 610 615 620
 Ala Glu Leu Gly Gly Cys Ile Ser Ala Pro Cys Ala His Gly Gly Thr
 625 630 635 640
 Cys Tyr Pro Gln Pro Ser Gly Tyr Asn Cys Thr Cys Pro Thr Gly Tyr
 645 650 655
 Thr Gly Pro Thr Cys Ser Glu Glu Met Thr Ala Cys His Ser Gly Pro
 660 665 670
 Cys Leu Asn Gly Gly Ser Cys Asn Pro Ser Pro Gly Gly Tyr Tyr Cys
 675 680 685
 Thr Cys Pro Pro Ser His Thr Gly Pro Gln Cys Gln Thr Ser Thr Asp
 690 695 700
 Tyr Cys Val Ser Ala Pro Cys Phe Asn Gly Gly Thr Cys Val Asn Arg
 705 710 715 720
 Pro Gly Thr Phe Ser Cys Leu Cys Ala Met Gly Phe Gln Gly Pro Arg
 725 730 735

Cys Glu Gly Lys Leu Arg Pro Ser Cys Ala Asp Ser Pro Cys Arg Asn
 740 745 750
 Arg Ala Thr Cys Gln Asp Ser Pro Gln Gly Pro Arg Cys Leu Cys Pro
 755 760 765
 Thr Gly Tyr Thr Gly Gly Ser Cys Gln Thr Leu Met Asp Leu Cys Ala
 770 775 780
 Gln Lys Pro Cys Pro Arg Asn Ser His Cys Leu Gln Thr Gly Pro Ser
 785 790 795 800
 Phe His Cys Leu Cys Leu Gln Gly Trp Thr Gly Pro Leu Cys Asn Leu
 805 810 815
 Pro Leu Ser Ser Cys Gln Lys Ala Ala Leu Ser Gln Gly Ile Asp Val
 820 825 830
 Ser Ser Leu Cys His Asn Gly Gly Leu Cys Val Asp Ser Gly Pro Ser
 835 840 845
 Tyr Phe Cys His Cys Pro Pro Gly Phe Gln Gly Ser Leu Cys Gln Asp
 850 855 860
 His Val Asn Pro Cys Glu Ser Arg Pro Cys Gln Asn Gly Ala Thr Cys
 865 870 875 880
 Met Ala Gln Pro Ser Gly Tyr Leu Cys Gln Cys Ala Pro Gly Tyr Asp
 885 890 895
 Gly Gln Asn Cys Ser Lys Glu Leu Asp Ala Cys Gln Ser Gln Pro Cys
 900 905 910
 His Asn His Gly Thr Cys Thr Pro Lys Pro Gly Gly Phe His Cys Ala
 915 920 925
 Cys Pro Pro Gly Phe Val Gly Leu Arg Cys Glu Gly Asp Val Asp Glu
 930 935 940
 Cys Leu Asp Gln Pro Cys His Pro Thr Gly Thr Ala Ala Cys His Ser
 945 950 955 960
 Leu Ala Asn Ala Phe Tyr Cys Gln Cys Leu Pro Gly His Thr Gly Gln
 965 970 975
 Trp Cys Glu Val Glu Ile Asp Pro Cys His Ser Gln Pro Cys Phe His
 980 985 990
 Gly Gly Thr Cys Glu Ala Thr Ala Gly Ser Pro Leu Gly Phe Ile Cys
 995 1000 1005
 His Cys Pro Lys Gly Phe Glu Gly Pro Thr Cys Ser His Arg Ala
 1010 1015 1020
 Pro Ser Cys Gly Phe His His Cys His His Gly Gly Leu Cys Leu
 1025 1030 1035

Pro Ser Pro Lys Pro Gly Phe Pro Pro Arg Cys Ala Cys Leu Ser
 1040 1045 1050
 Gly Tyr Gly Gly Pro Asp Cys Leu Thr Pro Pro Ala Pro Lys Gly
 1055 1060 1065
 Cys Gly Pro Pro Ser Pro Cys Leu Tyr Asn Gly Ser Cys Ser Glu
 1070 1075 1080
 Thr Thr Gly Leu Gly Gly Pro Gly Phe Arg Cys Ser Cys Pro His
 1085 1090 1095
 Ser Ser Pro Gly Pro Arg Cys Gln Lys Pro Gly Ala Lys Gly Cys
 1100 1105 1110
 Glu Gly Arg Ser Gly Asp Gly Ala Cys Asp Ala Gly Cys Ser Gly
 1115 1120 1125
 Pro Gly Gly Asn Trp Asp Gly Gly Asp Cys Ser Leu Gly Val Pro
 1130 1135 1140
 Asp Pro Trp Lys Gly Cys Pro Ser His Ser Arg Cys Trp Leu Leu
 1145 1150 1155
 Phe Arg Asp Gly Gln Cys His Pro Gln Cys Asp Ser Glu Glu Cys
 1160 1165 1170
 Leu Phe Asp Gly Tyr Asp Cys Glu Thr Pro Pro Ala Cys Thr Pro
 1175 1180 1185
 Ala Tyr Asp Gln Tyr Cys His Asp His Phe His Asn Gly His Cys
 1190 1195 1200
 Glu Lys Gly Cys Asn Thr Ala Glu Cys Gly Trp Asp Gly Gly Asp
 1205 1210 1215
 Cys Arg Pro Glu Asp Gly Asp Pro Glu Trp Gly Pro Ser Leu Ala
 1220 1225 1230
 Leu Leu Val Val Leu Ser Pro Pro Ala Leu Asp Gln Gln Leu Phe
 1235 1240 1245
 Ala Leu Ala Arg Val Leu Ser Leu Thr Leu Arg Val Gly Leu Trp
 1250 1255 1260
 Val Arg Lys Asp Arg Asp Gly Arg Asp Met Val Tyr Pro Tyr Pro
 1265 1270 1275
 Gly Ala Arg Ala Glu Glu Lys Leu Gly Gly Thr Arg Asp Pro Thr
 1280 1285 1290
 Tyr Gln Glu Arg Ala Ala Pro Gln Thr Gln Pro Leu Gly Lys Glu
 1295 1300 1305
 Thr Asp Ser Leu Ser Ala Gly Phe Val Val Val Met Gly Val Asp
 1310 1315 1320

Leu Ser Arg Cys Gly Pro Asp His Pro Ala Ser Arg Cys Pro Trp
1325 1330 1335

Asp Pro Gly Leu Leu Leu Arg Phe Leu Ala Ala Met Ala Ala Val
1340 1345 1350

Gly Ala Leu Glu Pro Leu Leu Pro Gly Pro Leu Leu Ala Val His
1355 1360 1365

Pro His Ala Gly Thr Ala Pro Pro Ala Asn Gln Leu Pro Trp Pro
1370 1375 1380

Val Leu Cys Ser Pro Val Ala Gly Val Ile Leu Leu Ala Leu Gly
1385 1390 1395

Ala Leu Leu Val Leu Gln Leu Ile Arg Arg Arg Arg Arg Glu His
1400 1405 1410

Gly Ala Leu Trp Leu Pro Pro Gly Phe Thr Arg Arg Pro Arg Thr
1415 1420 1425

Gln Ser Ala Pro His Arg Arg Arg Pro Pro Leu Gly Glu Asp Ser
1430 1435 1440

Ile Gly Leu Lys Ala Leu Lys Pro Lys Ala Glu Val Asp Glu Asp
1445 1450 1455

Gly Val Val Met Cys Ser Gly Pro Glu Glu Gly Glu Glu Val Gly
1460 1465 1470

Gln Ala Glu Glu Thr Gly Pro Pro Ser Thr Cys Gln Leu Trp Ser
1475 1480 1485

Leu Ser Gly Gly Cys Gly Ala Leu Pro Gln Ala Ala Met Leu Thr
1490 1495 1500

Pro Pro Gln Glu Ser Glu Met Glu Ala Pro Asp Leu Asp Thr Arg
1505 1510 1515

Gly Pro Asp Gly Val Thr Pro Leu Met Ser Ala Val Cys Cys Gly
1520 1525 1530

Glu Val Gln Ser Gly Thr Phe Gln Gly Ala Trp Leu Gly Cys Pro
1535 1540 1545

Glu Pro Trp Glu Pro Leu Leu Asp Gly Gly Ala Cys Pro Gln Ala
1550 1555 1560

His Thr Val Gly Thr Gly Glu Thr Pro Leu His Leu Ala Ala Arg
1565 1570 1575

Phe Ser Arg Pro Thr Ala Ala Arg Arg Leu Leu Glu Ala Gly Ala
1580 1585 1590

Asn Pro Asn Gln Pro Asp Arg Ala Gly Arg Thr Pro Leu His Ala
1595 1600 1605

Ala Val Ala Ala Asp Ala Arg Glu Val Cys Gln Leu Leu Leu Arg

1610	1615	1620
Ser Arg Gln Thr Ala Val Asp Ala Arg Thr Glu Asp Gly Thr Thr		
1625	1630	1635
Pro Leu Met Leu Ala Ala Arg Leu Ala Val Glu Asp Leu Val Glu		
1640	1645	1650
Glu Leu Ile Ala Ala Gln Ala Asp Val Gly Ala Arg Asp Lys Trp		
1655	1660	1665
Gly Lys Thr Ala Leu His Trp Ala Ala Ala Val Asn Asn Ala Arg		
1670	1675	1680
Ala Ala Arg Ser Leu Leu Gln Ala Gly Ala Asp Lys Asp Ala Gln		
1685	1690	1695
Asp Asn Arg Glu Gln Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly		
1700	1705	1710
Ala Val Glu Val Ala Gln Leu Leu Leu Gly Leu Gly Ala Ala Arg		
1715	1720	1725
Glu Leu Arg Asp Gln Ala Gly Leu Ala Pro Ala Asp Val Ala His		
1730	1735	1740
Gln Arg Asn His Trp Asp Leu Leu Thr Leu Leu Glu Gly Ala Gly		
1745	1750	1755
Pro Pro Glu Ala Arg His Lys Ala Thr Pro Gly Arg Glu Ala Gly		
1760	1765	1770
Pro Phe Pro Arg Ala Arg Thr Val Ser Val Ser Val Pro Pro His		
1775	1780	1785
Gly Gly Gly Ala Leu Pro Arg Cys Arg Thr Leu Ser Ala Gly Ala		
1790	1795	1800
Gly Pro Arg Gly Gly Gly Ala Cys Leu Gln Ala Arg Thr Trp Ser		
1805	1810	1815
Val Asp Leu Ala Ala Arg Gly Gly Gly Ala Tyr Ser His Cys Arg		
1820	1825	1830
Ser Leu Ser Gly Val Gly Ala Gly Gly Gly Pro Thr Pro Arg Gly		
1835	1840	1845
Arg Arg Phe Ser Ala Gly Met Arg Gly Pro Arg Pro Asn Pro Ala		
1850	1855	1860
Ile Met Arg Gly Arg Tyr Gly Val Ala Ala Gly Arg Gly Gly Arg		
1865	1870	1875
Val Ser Thr Asp Asp Trp Pro Cys Asp Trp Val Ala Leu Gly Ala		
1880	1885	1890
Cys Gly Ser Ala Ser Asn Ile Pro Ile Pro Pro Pro Cys Leu Thr		
1895	1900	1905

Pro Ser Pro Glu Arg Gly Ser Pro Gln Leu Asp Cys Gly Pro Pro
1910 1915 1920

Ala Leu Gln Glu Met Pro Ile Asn Gln Gly Gly Glu Gly Lys Lys
1925 1930 1935

<210> 123

<211> 759

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 123

Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
1 5 10 15

Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala Cys
20 25 30

Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
35 40 45

Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val Asp
50 55 60

Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
65 70 75 80

Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
85 90 95

Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
100 105 110

Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
115 120 125

Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
130 135 140

Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
145 150 155 160

Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
165 170 175

Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
180 185 190

Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
195 200 205

Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro
210 215 220

Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met

225 230 235 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
 245 250 255

Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
 260 265 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
 275 280 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
 290 295 300

Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305 310 315 320

Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His Val
 325 330 335

Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
 340 345 350

His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
 355 360 365

Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
370 375 380

Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
385 390 395 400

Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
 405 410 415

Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
 420 425 430

Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu
435 440 445

Val Met Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
450 455 460

Lys Val Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu
465 470 475 480

Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn
 485 490 495

Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys
 500 505 510

Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu
515 520 525

Leu Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys
530 535 540

Val Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly
545 550 555 560

Asp Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met
565 570 575

Ala Glu Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His
580 585 590

Ile Ala Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His
595 600 605

Phe Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn
610 615 620

Leu Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser
625 630 635 640

Thr Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp
645 650 655

Met Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp
660 665 670

Val Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys
675 680 685

Gln Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr
690 695 700

Gln Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr
705 710 715 720

Glu Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Met Arg Lys Asn
725 730 735

Ile Lys Gly Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro
740 745 750

Val Tyr Leu Asp Ile Leu Gly
755

<210> 124

<211> 816

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 124

Met Asp Val Ser Leu Cys Pro Ala Lys Cys Ser Phe Trp Arg Ile Phe
1 5 10 15

Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu Ala Cys
20 25 30

Pro Ala Asn Cys Val Cys Ser Lys Thr Glu Ile Asn Cys Arg Arg Pro

35 40 45
 Asp Asp Gly Asn Leu Phe Pro Leu Leu Glu Gly Gln Asp Ser Gly Asn
 50 55 60
 Ser Asn Gly Asn Ala Asn Ile Asn Ile Thr Asp Ile Ser Arg Asn Ile
 65 70 75 80
 Thr Ser Ile His Ile Glu Asn Trp Arg Ser Leu His Thr Leu Asn Ala
 85 90 95
 Val Asp Met Glu Leu Tyr Thr Gly Leu Gln Lys Leu Thr Ile Lys Asn
 100 105 110
 Ser Gly Leu Arg Ser Ile Gln Pro Arg Ala Phe Ala Lys Asn Pro His
 115 120 125
 Leu Arg Tyr Met Gln Leu Glu Gln Asn Phe Phe Asn Cys Ser Cys Asp
 130 135 140
 Ile Arg Trp Met Gln Leu Trp Gln Glu Gln Gly Glu Ala Lys Leu Asn
 145 150 155 160
 Ser Gln Asn Leu Tyr Cys Ile Asn Ala Asp Gly Ser Gln Leu Pro Leu
 165 170 175
 Phe Arg Met Asn Ile Ser Gln Cys Asp Leu Pro Glu Ile Ser Val Ser
 180 185 190
 His Val Asn Leu Thr Val Arg Glu Gly Asp Asn Ala Val Ile Thr Cys
 195 200 205
 Asn Gly Ser Gly Ser Pro Leu Pro Asp Val Asp Trp Ile Val Thr Gly
 210 215 220
 Leu Gln Ser Ile Asn Thr His Gln Thr Asn Leu Asn Trp Thr Asn Val
 225 230 235 240
 His Ala Ile Asn Leu Thr Leu Val Asn Val Thr Ser Glu Asp Asn Gly
 245 250 255
 Phe Thr Leu Thr Cys Ile Ala Glu Asn Val Val Gly Met Ser Asn Ala
 260 265 270
 Ser Val Ala Leu Thr Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu
 275 280 285
 Glu Pro Glu Leu Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly
 290 295 300
 Asn Pro Pro Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg
 305 310 315 320
 Glu Ser Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser
 325 330 335
 Glu Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn
 340 345 350

Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr Ile
355 360 365

Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp Asn Phe
370 375 380

Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr Val Thr His
385 390 395 400

Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala Val Gly Leu Ala
405 410 415

Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe Val Met Ile Asn Lys
420 425 430

Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys Gly Pro Val Ala Val Ile
435 440 445

Ser Gly Glu Glu Asp Ser Ala Ser Pro Leu His His Ile Asn His Gly
450 455 460

Ile Thr Thr Pro Ser Ser Leu Asp Ala Gly Pro Asp Thr Val Val Ile
465 470 475 480

Gly Met Thr Arg Ile Pro Val Ile Glu Asn Pro Gln Tyr Phe Arg Gln
485 490 495

Gly His Asn Cys His Lys Pro Asp Thr Tyr Val Gln His Ile Lys Arg
500 505 510

Arg Asp Ile Val Leu Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys
515 520 525

Val Phe Leu Ala Glu Cys Tyr Asn Leu Ser Pro Thr Lys Asp Lys Met
530 535 540

Leu Val Ala Val Lys Ala Leu Lys Asp Pro Thr Leu Ala Ala Arg Lys
545 550 555 560

Asp Phe Gln Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His
565 570 575

Ile Val Lys Phe Tyr Gly Val Cys Gly Asp Gly Asp Pro Leu Ile Met
580 585 590

Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg Ala
595 600 605

His Gly Pro Asp Ala Met Ile Leu Val Asp Gly Gln Pro Arg Gln Ala
610 615 620

Lys Gly Glu Leu Gly Leu Ser Gln Met Leu His Ile Ala Ser Gln Ile
625 630 635 640

Ala Ser Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg Asp
645 650 655

Leu Ala Thr Arg Asn Cys Leu Val Gly Ala Asn Leu Leu Val Lys Ile
660 665 670

Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp Tyr Tyr Arg
675 680 685

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu Val Gly
690 695 700

Gly His Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Met
705 710 715 720

Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Phe Gly Val Ile
725 730 735

Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Phe Gln Leu Ser
740 745 750

Asn Thr Glu Val Ile Glu Cys Ile Thr Gln Gly Arg Val Leu Glu Arg
755 760 765

Pro Arg Val Cys Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp
770 775 780

Gln Arg Glu Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile
785 790 795 800

Leu His Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly
805 810 815

<210> 125

<211> 662

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 125

Met Asp Val Ser Leu Cys Pro Ala Lys Cys Ser Phe Trp Arg Ile Phe
1 5 10 15

Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu Ala Cys
20 25 30

Pro Ala Asn Cys Val Cys Ser Lys Thr Glu Ile Asn Cys Arg Arg Pro
35 40 45

Asp Asp Gly Asn Leu Phe Pro Leu Leu Glu Gly Gln Asp Ser Gly Asn
50 55 60

Ser Asn Gly Asn Ala Asn Ile Asn Ile Thr Asp Ile Ser Arg Asn Ile
65 70 75 80

Thr Ser Ile His Ile Glu Asn Trp Arg Ser Leu His Thr Leu Asn Ala
85 90 95

Val Asp Met Glu Leu Tyr Thr Gly Leu Gln Lys Leu Thr Ile Lys Asn
100 105 110

Ser Gly Leu Arg Ser Ile Gln Pro Arg Ala Phe Ala Lys Asn Pro His
115 120 125

Leu Arg Tyr Ile Asn Leu Ser Ser Asn Arg Leu Thr Thr Leu Ser Trp
130 135 140

Gln Leu Phe Gln Thr Leu Ser Leu Arg Glu Leu Gln Leu Glu Gln Asn
145 150 155 160

Phe Phe Asn Cys Ser Cys Asp Ile Arg Trp Met Gln Leu Trp Gln Glu
165 170 175

Gln Gly Glu Ala Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala
180 185 190

Asp Gly Ser Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp
195 200 205

Leu Pro Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly
210 215 220

Asp Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp
225 230 235 240

Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln Thr
245 250 255

Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu Val Asn
260 265 270

Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile Ala Glu Asn
275 280 285

Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr Val Tyr Tyr Pro
290 295 300

Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu Arg Leu Glu His Cys
305 310 315 320

Ile Glu Phe Val Val Arg Gly Asn Pro Pro Pro Thr Leu His Trp Leu
325 330 335

His Asn Gly Gln Pro Leu Arg Glu Ser Lys Ile Ile His Val Glu Tyr
340 345 350

Tyr Gln Glu Gly Glu Ile Ser Glu Gly Cys Leu Leu Phe Asn Lys Pro
355 360 365

Thr His Tyr Asn Asn Gly Asn Tyr Thr Leu Ile Ala Lys Asn Pro Leu
370 375 380

Gly Thr Ala Asn Gln Thr Ile Asn Gly His Phe Leu Lys Glu Pro Phe
385 390 395 400

Pro Glu Ser Thr Asp Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr
405 410 415

Pro Pro Ile Thr Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val
 420 425 430
 Ser Ile Ala Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val
 435 440 445
 Leu Phe Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met
 450 455 460
 Lys Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro
 465 470 475 480
 Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp Ala
 485 490 495
 Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val Ile Glu
 500 505 510
 Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys Pro Asp Thr
 515 520 525
 Tyr Val Gln His Ile Lys Arg Arg Asp Ile Val Leu Lys Arg Glu Leu
 530 535 540
 Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu
 545 550 555 560
 Ser Pro Thr Lys Asp Lys Met Leu Val Ala Val Lys Ala Leu Lys Asp
 565 570 575
 Pro Thr Leu Ala Ala Arg Lys Asp Phe Gln Arg Glu Ala Glu Leu Leu
 580 585 590
 Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Gly
 595 600 605
 Asp Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
 610 615 620
 Leu Asn Lys Phe Leu Arg Trp Glu Asp Thr Pro Cys Ser Pro Phe Ala
 625 630 635 640
 Gly Cys Leu Leu Lys Ala Ser Cys Thr Gly Ser Ser Leu Gln Arg Val
 645 650 655
 Met Tyr Gly Ala Ser Gly
 660
 <210> 126
 <211> 437
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 126
 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Asp
 100 105 110
 Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp
 115 120 125
 Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser
 130 135 140
 Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn
 145 150 155 160
 Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro
 165 170 175
 Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala
 180 185 190
 Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu
 195 200 205
 Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr
 210 215 220
 Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln
 225 230 235 240
 Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp
 245 250 255
 Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn
 260 265 270
 Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser
 275 280 285
 Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe
 290 295 300
 Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly
 305 310 315 320

Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr
325 330 335

Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro
340 345 350

Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala
355 360 365

Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His
370 375 380

Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser
385 390 395 400

Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu
405 410 415

Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser
420 425 430

Leu Thr Glu Thr Ser
435

<210> 127

<211> 436

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 127

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr
1 5 10 15

Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
20 25 30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
35 40 45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
50 55 60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65 70 75 80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
100 105 110

His Leu Gly Leu Thr Glu Gly Thr Gly Ala Asp Pro Val Val Ser Ala
115 120 125

Lys Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp
130 135 140

Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu
145 150 155 160

Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu
165 170 175

Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu
180 185 190

Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr
195 200 205

Ile Leu Pro Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu
210 215 220

Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu
225 230 235 240

Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser
245 250 255

Cys Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met
260 265 270

Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly
275 280 285

Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu
290 295 300

Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu
305 310 315 320

Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser
325 330 335

Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys
340 345 350

Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr
355 360 365

Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala
370 375 380

Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn
385 390 395 400

Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser
405 410 415

Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu
420 425 430

Lys Gln Ala Leu
435

<210> 128
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 128

Met Glu Ser His Ser Arg Ala Gly Lys Ser Arg Lys Ser Ala Lys Phe
1 5 10 15

Arg Ser Ile Ser Arg Ser Leu Met Leu Cys Asn Ala Lys Thr Ser Asp
20 25 30

Asp Gly Ser Ser Pro Asp Glu Lys Tyr Pro Asp Pro Phe Glu Ile Ser
35 40 45

Leu Ala Gln Gly Lys Glu Gly Ile Phe His Ser Ser Val Gln Leu Ala
50 55 60

Asp Thr Ser Glu Ala Gly Pro Ser Ser Val Pro Asp Leu Ala Leu Ala
65 70 75 80

Ser Glu Ala Ala Gln Leu Gln Ala Ala Gly Asn Asp Arg Gly Lys Thr
85 90 95

Cys Arg Arg Ile Phe Phe Met Val Leu Ile Pro Ile Ala Gln Glu Lys
100 105 110

Leu Ile Phe Gln
115

<210> 129
<211> 1210
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 129

Met Glu Ser His Ser Arg Ala Gly Lys Ser Arg Lys Ser Ala Lys Phe
1 5 10 15

Arg Ser Ile Ser Arg Ser Leu Met Leu Cys Asn Ala Lys Thr Ser Asp
20 25 30

Asp Gly Ser Ser Pro Asp Glu Lys Tyr Pro Asp Pro Phe Glu Ile Ser
35 40 45

Leu Ala Gln Gly Lys Glu Gly Ile Phe His Ser Ser Val Gln Leu Ala
50 55 60

Asp Thr Ser Glu Ala Gly Pro Ser Ser Val Pro Asp Leu Ala Leu Ala
65 70 75 80

Ser Glu Ala Ala Gln Leu Gln Ala Ala Gly Asn Asp Arg Gly Lys Thr
85 90 95

Cys Arg Arg Ile Phe Phe Met Lys Glu Ser Ser Thr Ala Ser Ser Arg
100 105 110

Glu Lys Pro Gly Lys Leu Glu Ala Gln Ser Ser Asn Phe Leu Phe Pro
115 120 125

Lys Ala Cys His Gln Arg Ala Arg Ser Asn Ser Thr Ser Val Asn Pro
130 135 140

Tyr Cys Thr Arg Glu Ile Asp Phe Pro Met Thr Lys Lys Ser Ala Ala
145 150 155 160

Pro Thr Asp Arg Gln Pro Tyr Ser Leu Cys Ser Asn Arg Lys Ser Leu
165 170 175

Ser Gln Gln Leu Asp Cys Pro Ala Gly Lys Ala Ala Gly Thr Ser Arg
180 185 190

Pro Thr Arg Ser Leu Ser Thr Ala Gln Leu Val Gln Pro Ser Gly Gly
195 200 205

Leu Gln Ala Ser Val Ile Ser Asn Ile Val Leu Met Lys Gly Gln Ala
210 215 220

Lys Gly Leu Gly Phe Ser Ile Val Gly Gly Lys Asp Ser Ile Tyr Gly
225 230 235 240

Pro Ile Gly Ile Tyr Val Lys Thr Ile Phe Ala Gly Gly Ala Ala Ala
245 250 255

Ala Asp Gly Arg Leu Gln Glu Gly Asp Glu Ile Leu Glu Leu Asn Gly
260 265 270

Glu Ser Met Ala Gly Leu Thr His Gln Asp Ala Leu Gln Lys Phe Lys
275 280 285

Gln Ala Lys Lys Gly Leu Leu Thr Leu Thr Val Arg Thr Arg Leu Thr
290 295 300

Ala Pro Pro Ser Leu Cys Ser His Leu Ser Pro Pro Leu Cys Arg Ser
305 310 315 320

Leu Ser Ser Ser Thr Cys Ile Thr Lys Asp Ser Ser Ser Phe Ala Leu
325 330 335

Glu Ser Pro Ser Ala Pro Ile Ser Thr Ala Lys Pro Asn Tyr Arg Ile
340 345 350

Met Val Glu Val Ser Leu Gln Lys Glu Ala Gly Val Gly Leu Gly Ile
355 360 365

Gly Leu Cys Ser Val Pro Tyr Phe Gln Cys Ile Ser Gly Ile Phe Val
370 375 380

His Thr Leu Ser Pro Gly Ser Val Ala His Leu Asp Gly Arg Leu Arg
385 390 395 400

Cys Gly Asp Glu Ile Val Glu Ile Ser Asp Ser Pro Val His Cys Leu

405 410 415
 Thr Leu Asn Glu Val Tyr Thr Ile Leu Ser His Cys Asp Pro Gly Pro
 420 425 430
 Val Pro Ile Ile Val Ser Arg His Pro Asp Pro Gln Val Ser Glu Gln
 435 440 445
 Gln Leu Lys Glu Ala Val Ala Gln Ala Val Glu Asn Thr Lys Phe Gly
 450 455 460
 Lys Glu Arg His Gln Trp Ser Leu Glu Gly Val Lys Arg Leu Glu Ser
 465 470 475 480
 Ser Trp His Gly Arg Pro Thr Leu Glu Lys Glu Arg Glu Lys Asn Ser
 485 490 495
 Ala Pro Pro His Arg Arg Ala Gln Lys Val Met Ile Arg Ser Ser Ser
 500 505 510
 Asp Ser Ser Tyr Met Ser Gly Ser Pro Gly Gly Ser Pro Gly Ser Gly
 515 520 525
 Ser Ala Glu Lys Pro Ser Ser Asp Val Asp Ile Ser Thr His Ser Pro
 530 535 540
 Ser Leu Pro Leu Ala Arg Glu Pro Val Val Leu Ser Ile Ala Ser Ser
 545 550 555 560
 Arg Leu Pro Gln Glu Ser Pro Pro Leu Pro Glu Ser Arg Asp Ser His
 565 570 575
 Pro Pro Leu Arg Leu Lys Lys Ser Phe Glu Ile Leu Glu Ala Arg Glu
 580 585 590
 Leu Leu Pro Leu Leu Leu Pro Gln Glu Asp Thr Ala Gly Arg Ser Pro
 595 600 605
 Ser Ala Ser Ala Gly Cys Pro Gly Pro Gly Ile Gly Pro Gln Thr Lys
 610 615 620
 Ser Ser Thr Glu Gly Glu Pro Gly Trp Arg Arg Ala Ser Pro Val Thr
 625 630 635 640
 Gln Thr Ser Pro Ile Lys His Pro Leu Leu Lys Arg Gln Ala Arg Met
 645 650 655
 Asp Tyr Ser Phe Asp Thr Thr Ala Glu Asp Pro Trp Val Arg Ile Ser
 660 665 670
 Asp Cys Ile Lys Asn Leu Phe Ser Pro Ile Met Ser Glu Asn His Gly
 675 680 685
 His Met Pro Leu Gln Pro Asn Ala Ser Leu Asn Glu Glu Glu Gly Thr
 690 695 700
 Gln Gly His Pro Asp Gly Thr Pro Pro Lys Leu Asp Thr Ala Asn Gly
 705 710 715 720

Thr Pro Lys Val Tyr Lys Ser Ala Asp Ser Ser Thr Val Lys Lys Gly
725 730 735

Pro Pro Val Ala Pro Lys Pro Ala Trp Phe Arg Gln Ser Leu Lys Gly
740 745 750

Leu Arg Asn Arg Ala Ser Asp Pro Arg Gly Leu Pro Asp Pro Ala Leu
755 760 765

Ser Thr Gln Pro Ala Pro Ala Ser Arg Glu His Leu Gly Ser His Ile
770 775 780

Arg Ala Ser Ser Ser Ser Ser Ile Arg Gln Arg Ile Ser Ser Phe
785 790 795 800

Glu Thr Phe Gly Ser Ser Gln Leu Pro Asp Lys Gly Ala Gln Arg Leu
805 810 815

Ser Leu Gln Pro Ser Ser Gly Glu Ala Ala Lys Pro Leu Gly Lys His
820 825 830

Glu Glu Gly Arg Phe Ser Gly Leu Leu Gly Arg Gly Ala Ala Pro Thr
835 840 845

Leu Val Pro Gln Gln Pro Glu Gln Val Leu Ser Ser Gly Ser Pro Ala
850 855 860

Ala Ser Glu Ala Arg Asp Pro Gly Val Ser Glu Ser Pro Pro Pro Gly
865 870 875 880

Arg Gln Pro Asn Gln Lys Thr Leu Pro Pro Gly Pro Asp Pro Leu Leu
885 890 895

Arg Leu Leu Ser Thr Gln Ala Glu Glu Ser Gln Gly Pro Val Leu Lys
900 905 910

Met Pro Ser Gln Arg Ala Arg Ser Phe Pro Leu Thr Arg Ser Gln Ser
915 920 925

Cys Glu Thr Lys Leu Leu Asp Glu Lys Thr Ser Lys Leu Tyr Ser Ile
930 935 940

Ser Ser Gln Val Ser Ser Ala Val Met Lys Ser Leu Leu Cys Leu Pro
945 950 955 960

Ser Ser Ile Ser Cys Ala Gln Thr Pro Cys Ile Pro Lys Glu Gly Ala
965 970 975

Ser Pro Thr Ser Ser Ser Asn Glu Asp Ser Ala Ala Asn Gly Ser Ala
980 985 990

Glu Thr Ser Ala Leu Asp Thr Gly Phe Ser Leu Asn Leu Ser Glu Leu
995 1000 1005

Arg Glu Tyr Thr Glu Gly Leu Thr Glu Ala Lys Glu Asp Asp Asp
1010 1015 1020

Gly Asp His Ser Ser Leu Gln Ser Gly Gln Ser Val Ile Ser Leu
1025 1030 1035

Leu Ser Ser Glu Glu Leu Lys Lys Leu Ile Glu Glu Val Lys Val
1040 1045 1050

Leu Asp Glu Ala Thr Leu Lys Val His Arg Val Phe Pro Asn Gly
1055 1060 1065

Leu Ala Ser Gln Glu Gly Thr Ile Gln Lys Gly Asn Glu Val Leu
1070 1075 1080

Ser Ile Asn Gly Lys Ser Leu Lys Gly Thr Thr His His Asp Ala
1085 1090 1095

Leu Ala Ile Leu Arg Gln Ala Arg Glu Pro Arg Gln Ala Val Ile
1100 1105 1110

Val Thr Arg Lys Leu Thr Pro Glu Ala Met Pro Asp Leu Asn Ser
1115 1120 1125

Ser Thr Asp Ser Ala Ala Ser Ala Ser Ala Ala Ser Asp Val Ser
1130 1135 1140

Val Glu Ser Thr Ala Glu Ala Thr Val Cys Thr Val Thr Leu Glu
1145 1150 1155

Lys Met Ser Ala Gly Leu Gly Phe Ser Leu Glu Gly Gly Lys Gly
1160 1165 1170

Ser Leu His Gly Asp Lys Pro Leu Thr Ile Asn Arg Ile Phe Lys
1175 1180 1185

Gly Gly His Arg Gly Leu Arg Ala Arg Gly Lys Ile Pro Val Asn
1190 1195 1200

Ile Val Ala Gln Lys Ser His
1205 1210

<210> 130
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 130

Met Leu Pro Leu Cys Leu Val Ala Ala Leu Leu Ala Ala Gly Pro
1 5 10 15

Gly Pro Ser Leu Gly Asp Glu Ala Ile His Cys Pro Pro Cys Ser Glu
20 25 30

Glu Lys Leu Ala Arg Cys Arg Pro Pro Val Gly Cys Glu Glu Leu Val
35 40 45

Arg Glu Pro Gly Cys Gly Cys Cys Ala Thr Cys Ala Leu Gly Leu Gly
50 55 60

Met Pro Cys Gly Val Tyr Thr Pro Arg Cys Gly Ser Gly Leu Arg Cys
65 70 75 80

Tyr Pro Pro Arg Gly Val Glu Lys Pro Leu His Thr Leu Met His Gly
85 90 95

Gln Gly Val Cys Met Glu Leu Ala Glu Ile Glu Ala Ile Gln Glu Ser
100 105 110

Leu Gln Pro Ser Asp Lys Asp Glu Gly Asp His Pro Asn Asn Ser Phe
115 120 125

Ser Pro Cys Ser Ala His Asp Arg Arg Cys Leu Gln Lys His Phe Ala
130 135 140

Lys Ile Arg Asp Arg Ser Thr Ser Gly Gly Lys Met Lys Val Asn Gly
145 150 155 160

Ala Pro Arg Glu Asp Ala Arg Pro Val Cys His Pro Ala Leu Asp Gly
165 170 175

Gln Arg Gly Lys Cys Trp Cys Val Asp Arg Lys Thr Gly Val Lys Leu
180 185 190

Pro Gly Gly Leu Glu Pro Lys Gly Glu Leu Asp Cys His Gln Leu Ala
195 200 205

Asp Ser Phe Arg Glu
210

<210> 131

<211> 871

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 131

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu
1 5 10 15

Ala Pro Ala Gly Ala Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys
20 25 30

Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
35 40 45

His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
50 55 60

Gln Arg Ile Met Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
65 70 75 80

Asp Cys Lys Tyr Asp Tyr Val Glu Val Phe Asp Gly Glu Asn Glu Asn
85 90 95

Gly His Phe Arg Gly Lys Phe Cys Gly Lys Ile Ala Pro Pro Pro Val

100 105 110
 Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
 115 120 125
 Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
 130 135 140
 Pro Glu Cys Ser Gln Asn Tyr Thr Thr Pro Ser Gly Val Ile Lys Ser
 145 150 155 160
 Pro Gly Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile
 165 170 175
 Val Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
 180 185 190
 Asp Leu Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
 195 200 205
 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Asp Asp Phe Lys Cys Met
 210 215 220
 Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser Asp Gln Ile Thr
 225 230 235 240
 Ala Ser Ser Gln Tyr Ser Thr Asn Trp Ser Ala Glu Arg Ser Arg Leu
 245 250 255
 Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp Ser Tyr Arg Glu
 260 265 270
 Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val Thr Ala Val Gly
 275 280 285
 Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys Tyr Tyr Val Lys
 290 295 300
 Thr Tyr Lys Ile Asp Val Ser Ser Asn Gly Glu Asp Trp Ile Thr Ile
 305 310 315 320
 Lys Glu Gly Asn Lys Pro Val Leu Phe Gln Gly Asn Thr Asn Pro Thr
 325 330 335
 Asp Val Val Val Ala Val Phe Pro Lys Pro Leu Ile Thr Arg Phe Val
 340 345 350
 Arg Ile Lys Pro Ala Thr Trp Glu Thr Gly Ile Ser Met Arg Phe Glu
 355 360 365
 Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser Gly Met Leu Gly
 370 375 380
 Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr Ser Ser Asn Gln
 385 390 395 400
 Gly Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu Val Thr Ser Arg
 405 410 415

Ser Gly Trp Ala Leu Pro Pro Ala Pro His Ser Tyr Ile Asn Glu Trp
 420 425 430
 Leu Gln Ile Asp Leu Gly Glu Glu Lys Ile Val Arg Gly Ile Ile Ile
 435 440 445
 Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met Arg Lys Phe Lys
 450 455 460
 Ile Gly Tyr Ser Asn Asn Gly Ser Asp Trp Lys Met Ile Met Asp Asp
 465 470 475 480
 Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn Asn Tyr Asp Thr
 485 490 495
 Pro Glu Leu Arg Thr Phe Pro Ala Leu Ser Thr Arg Phe Ile Arg Ile
 500 505 510
 Tyr Pro Glu Arg Ala Thr His Gly Gly Leu Gly Leu Arg Met Glu Leu
 515 520 525
 Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro Thr Thr Pro Asn
 530 535 540
 Gly Asn Leu Val Asp Glu Cys Asp Asp Asp Gln Ala Asn Cys His Ser
 545 550 555 560
 Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr Thr Val Leu Ala
 565 570 575
 Thr Glu Lys Pro Thr Val Ile Asp Ser Thr Ile Gln Ser Glu Phe Pro
 580 585 590
 Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser His Lys Thr Phe
 595 600 605
 Cys His Trp Glu His Asp Asn His Val Gln Leu Lys Trp Ser Val Leu
 610 615 620
 Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly Asp Gly Asn Phe
 625 630 635 640
 Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys Val Ala Arg Leu
 645 650 655
 Val Ser Pro Val Val Tyr Ser Gln Asn Ser Ala His Cys Met Thr Phe
 660 665 670
 Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu Arg Val Lys Leu
 675 680 685
 Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val Trp Met Ala Ile
 690 695 700
 Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val Leu Leu His Lys
 705 710 715 720

Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu Ile Gly Lys Gly
725 730 735

Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile Asn Asn His Ile
740 745 750

Ser Gln Glu Asp Cys Ala Lys Pro Ala Asp Leu Asp Lys Lys Asn Pro
755 760 765

Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly Tyr Glu Gly Glu
770 775 780

Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly Asn Val Leu Lys
785 790 795 800

Thr Leu Glu Pro Ile Leu Ile Thr Ile Ile Ala Met Ser Ala Leu Gly
805 810 815

Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr Cys Ala Cys Trp
820 825 830

His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu Glu Asn Tyr Asn
835 840 845

Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp Lys Leu Asn Thr
850 855 860

Gln Ser Thr Tyr Ser Glu Ala
865 870

<210> 132

<211> 110

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 132

Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala
1 5 10 15

Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
20 25 30

Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
35 40 45

Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
50 55 60

Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
65 70 75 80

Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Lys Thr Asn
85 90 95

Pro Arg Val Cys Ile Gln Arg Thr Val Arg Arg Lys Leu Val
100 105 110

<210> 133
 <211> 111
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 133

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu
 1 5 10 15

Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser
 20 25 30

Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu
 35 40 45

Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly
 50 55 60

Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg
 65 70 75 80

Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly
 85 90 95

Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Lys Arg Ile
 100 105 110

<210> 134
 <211> 35
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 134

Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Trp Leu Pro Arg
 1 5 10 15

Arg Thr Trp Thr Ser Ala Ala Ser Thr Trp Arg Thr Arg Arg Gly Leu
 20 25 30

Gly Thr Met
 35

<210> 135
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 135

Met Tyr Ser Ala Pro Ser Ala Cys Thr Cys Leu Cys Leu His Phe Leu
 1 5 10 15

Leu Leu Cys Phe Gln Val Gln Val Leu Val Ala Glu Glu Asn Val Asp

20 25 30

Phe Arg Ile His Val Glu Asn Gln Thr Arg Ala Arg Asp Asp Val Ser
35 40 45

Arg Lys Gln Leu Arg Leu Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys
50 55 60

His Ile Gln Val Leu Gly Arg Arg Ile Ser Ala Arg Gly Glu Asp Gly
65 70 75 80

Asp Lys Tyr Ala Arg Trp His Gln Gln Gly Val Trp Val His Arg Glu
85 90 95

Gly Ser Gly Glu Gln Leu His Gly Pro Asp Val Gly
100 105

<210> 136
<211> 287
<212> PRT
<213> Artificial sequence
<220>
<223> A novel predicted alternative spliced variant protein product
<400> 136

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
1 5 10 15

Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
20 25 30

Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
50 55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
225 230 235 240

Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
245 250 255

Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Gly Val Leu
260 265 270

Gln Tyr Gly Cys Gln Trp Gly Arg Leu Asp Cys Asn Thr Thr Ser
275 280 285

<210> 137

<211> 464

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 137

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
1 5 10 15

Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
20 25 30

Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
50 55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
225 230 235 240

Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
245 250 255

Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
260 265 270

Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
275 280 285

Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
290 295 300

Asn Asn Met Pro Glu Pro Lys Lys Gly Phe Gly Asn Pro Ser Gly Glu
305 310 315 320

Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln
325 330 335

Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr
340 345 350

Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg
355 360 365

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu
370 375 380

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn
385 390 395 400

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp
405 410 415

Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln
420 425 430

Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro
435 440 445

Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
450 455 460

<210> 138
 <211> 404
 <212> PRT
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant protein product

<400> 138

Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
 1 5 10 15

Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
 20 25 30

Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
 65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
 85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
 100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
 115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
 130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
 145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
 165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
 180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
 195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
 210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
 225 230 235 240

Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
 245 250 255

Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
 260 265 270

Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
275 280 285

Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
290 295 300

Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
305 310 315 320

Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
325 330 335

Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
340 345 350

Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
355 360 365

Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
370 375 380

Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
385 390 395 400

Tyr Arg Met Trp

<210> 139
<211> 226
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 139

Met Gln Pro Pro Pro Ser Leu Cys Gly Arg Ala Leu Val Ala Leu Val
1 5 10 15

Leu Ala Cys Gly Leu Ser Arg Ile Trp Gly Glu Glu Arg Gly Phe Pro
20 25 30

Pro Asp Arg Ala Thr Pro Leu Leu Gln Thr Ala Glu Ile Met Thr Pro
35 40 45

Pro Thr Lys Thr Leu Trp Pro Lys Gly Ser Asn Ala Ser Leu Ala Arg
50 55 60

Ser Leu Ala Pro Ala Glu Val Pro Lys Gly Asp Arg Thr Ala Gly Ser
65 70 75 80

Pro Pro Arg Thr Ile Ser Pro Pro Pro Cys Gln Gly Pro Ile Glu Ile
85 90 95

Lys Glu Thr Phe Lys Tyr Ile Asn Thr Val Val Ser Cys Leu Val Phe
100 105 110

Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lys
115 120 125

Asn Lys Cys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala
130 135 140

Leu Gly Asp Leu Leu His Ile Val Ile Asp Ile Pro Ile Asn Val Tyr
145 150 155 160

Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu
165 170 175

Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu
180 185 190

Cys Ala Leu Ser Ile Asp Ser Phe Thr Arg Gln Gln Lys Ile Gly Gly
195 200 205

Tyr Ser Val Ser Ile Ser Ala Cys His Trp Pro Ser Leu His Phe Phe
210 215 220

Ile His
225

<210> 140

<211> 741

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 140

Met Arg Gly Val Trp Pro Pro Pro Val Ser Ala Leu Leu Ser Ala Leu
1 5 10 15

Gly Val Asn Phe His Ser Pro Arg Ser Gly Gln Arg Cys Trp Ala Ala
20 25 30

Arg Thr Gln Val Glu Lys Arg Leu Val Val Leu Val Val Leu Leu Ala
35 40 45

Ala Gly Leu Val Ala Cys Leu Ala Ala Leu Gly Ile Gln Tyr Gln Thr
50 55 60

Arg Ser Pro Ser Val Cys Leu Ser Glu Ala Cys Val Ser Val Thr Ser
65 70 75 80

Ser Ile Leu Ser Ser Met Asp Pro Thr Val Asp Pro Cys His Asp Phe
85 90 95

Phe Ser Tyr Ala Cys Gly Gly Trp Ile Lys Ala Asn Pro Val Pro Asp
100 105 110

Gly His Ser Arg Trp Gly Thr Phe Ser Asn Leu Trp Glu His Asn Gln
115 120 125

Ala Ile Ile Lys His Leu Leu Glu Asn Ser Thr Ala Ser Val Ser Glu
130 135 140

Ala Glu Arg Lys Ala Gln Val Tyr Tyr Arg Ala Cys Met Asn Glu Thr

145 150 155 160
Arg Ile Glu Glu Leu Arg Ala Lys Pro Leu Met Glu Leu Ile Glu Arg
 165 170 175
Leu Gly Gly Trp Asn Ile Thr Gly Pro Trp Ala Lys Asp Asn Phe Gln
 180 185 190
Asp Thr Leu Gln Val Val Thr Ala His Tyr Arg Thr Ser Pro Phe Phe
 195 200 205
Ser Val Tyr Val Ser Ala Asp Ser Lys Asn Ser Asn Ser Asn Val Ile
 210 215 220
Gln Val Asp Gln Ser Gly Leu Gly Leu Pro Ser Arg Asp Tyr Tyr Leu
 225 230 235 240
Asn Lys Thr Glu Asn Glu Lys Val Leu Thr Gly Tyr Leu Asn Tyr Met
 245 250 255
Val Gln Leu Gly Lys Leu Leu Gly Gly Gly Asp Glu Glu Ala Ile Arg
 260 265 270
Pro Gln Met Gln Gln Ile Leu Asp Phe Glu Thr Ala Leu Ala Asn Ile
 275 280 285
Thr Ile Pro Gln Glu Lys Arg Arg Asp Glu Glu Leu Ile Tyr His Lys
 290 295 300
Val Thr Ala Ala Glu Leu Gln Thr Leu Ala Pro Ala Ile Asn Trp Leu
 305 310 315 320
Pro Phe Leu Asn Thr Ile Phe Tyr Pro Val Glu Ile Asn Glu Ser Glu
 325 330 335
Pro Ile Val Val Tyr Asp Lys Glu Tyr Leu Glu Gln Ile Ser Thr Leu
 340 345 350
Ile Asn Thr Thr Asp Arg Cys Leu Leu Asn Asn Tyr Met Ile Trp Asn
 355 360 365
Leu Val Arg Lys Thr Ser Ser Phe Leu Asp Gln Arg Phe Gln Asp Ala
 370 375 380
Asp Glu Lys Phe Met Glu Val Met Tyr Gly Thr Lys Lys Thr Cys Leu
 385 390 395 400
Pro Arg Trp Lys Phe Cys Val Ser Asp Thr Glu Asn Asn Leu Gly Phe
 405 410 415
Ala Leu Gly Pro Met Phe Val Lys Ala Thr Phe Ala Glu Asp Ser Lys
 420 425 430
Ser Ile Ala Thr Glu Ile Ile Leu Glu Ile Lys Lys Ala Phe Glu Glu
 435 440 445
Ser Leu Ser Thr Leu Lys Trp Met Asp Glu Glu Thr Arg Lys Ser Ala
 450 455 460

Lys Glu Lys Ala Asp Ala Ile Tyr Asn Met Ile Gly Tyr Pro Asn Phe
465 470 475 480

Ile Met Asp Pro Lys Glu Leu Asp Lys Val Phe Asn Asp Tyr Thr Ala
485 490 495

Val Pro Asp Leu Tyr Phe Glu Asn Ala Met Arg Phe Phe Asn Phe Ser
500 505 510

Trp Arg Val Thr Ala Asp Gln Leu Arg Lys Ala Pro Asn Arg Asp Gln
515 520 525

Trp Ser Met Thr Pro Pro Met Val Asn Ala Tyr Tyr Ser Pro Thr Lys
530 535 540

Asn Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Thr
545 550 555 560

Arg Ser Ser Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val Val
565 570 575

Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp
580 585 590

Lys Asp Gly Asn Leu Arg Pro Trp Trp Lys Asn Ser Ser Val Glu Ala
595 600 605

Phe Lys Arg Gln Thr Glu Cys Met Val Glu Gln Tyr Ser Asn Tyr Ser
610 615 620

Val Asn Gly Glu Pro Val Asn Gly Arg His Thr Leu Gly Glu Asn Ile
625 630 635 640

Ala Asp Asn Gly Gly Leu Lys Ala Ala Tyr Arg Ala Tyr Gln Asn Trp
645 650 655

Val Lys Lys Asn Gly Ala Glu His Ser Leu Pro Thr Leu Gly Leu Thr
660 665 670

Asn Asn Gln Leu Phe Phe Leu Gly Phe Ala Gln Val Trp Cys Ser Val
675 680 685

Arg Thr Pro Glu Ser Ser His Glu Gly Leu Ile Thr Asp Pro His Ser
690 695 700

Pro Ser Arg Phe Arg Val Ile Gly Ser Leu Ser Asn Ser Lys Glu Phe
705 710 715 720

Ser Glu His Phe Arg Cys Pro Pro Gly Ser Pro Met Asn Pro Pro His
725 730 735

Lys Cys Glu Val Trp
740

<210> 141

<211> 736

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 141

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Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Val Gly Phe
 1           5           10           15

Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu Glu Leu
 20           25           30

Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu Leu Gly Cys
 35           40           45

Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro Ser His Ser Thr
 50           55           60

Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly Lys Ile Leu Glu Ser
 65           70           75           80

Leu Asp Arg Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys
 85           90           95

Gly Gly Trp Ile Arg Arg Asn Pro Leu Pro Asp Gly Arg Ser Arg Trp
100           105           110

Asn Thr Phe Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His
115           120           125

Leu Leu Glu Asn Thr Thr Phe Asn Ser Ser Ser Glu Ala Glu Gln Lys
130           135           140

Thr Gln Arg Phe Tyr Leu Ser Cys Leu Gln Val Glu Arg Ile Glu Glu
145           150           155           160

Leu Gly Ala Gln Pro Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp
165           170           175

Asn Ile Thr Gly Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys
180           185           190

Ala Val Ala Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile
195           200           205

Ser Ala Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln
210           215           220

Ser Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala
225           230           235           240

Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu Gly
245           250           255

Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met Gln Gln
260           265           270

Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val Pro Gln Asp
275           280           285

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Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met Ser Ile Ser Glu
 290 295 300
 Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe
 305 310 315 320
 Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr
 325 330 335
 Gly Met Asp Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu
 340 345 350
 Pro Ser Ile Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr
 355 360 365
 Thr Ser Ser Leu Asp Arg Arg Phe Glu Ser Ala Gln Glu Lys Leu Leu
 370 375 380
 Glu Thr Leu Tyr Gly Thr Lys Lys Ser Cys Val Pro Arg Trp Gln Thr
 385 390 395 400
 Cys Ile Ser Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu
 405 410 415
 Phe Val Lys Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly
 420 425 430
 Met Ile Ser Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu
 435 440 445
 Val Trp Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp
 450 455 460
 Ala Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys
 465 470 475 480
 Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser Phe
 485 490 495
 Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val Met Ala
 500 505 510
 Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser Met Thr Pro
 515 520 525
 Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn Glu Ile Val Phe
 530 535 540
 Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala Arg Asn His Pro Lys
 545 550 555 560
 Ala Leu Asn Phe Gly Gly Ile Gly Val Val Met Gly His Glu Leu Thr
 565 570 575
 His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Glu Gly Asn Leu
 580 585 590

Arg Pro Trp Trp Gln Asn Glu Ser Leu Ala Ala Phe Arg Asn His Thr
595 600 605

Ala Cys Met Glu Glu Gln Tyr Asn Gln Tyr Gln Val Asn Gly Glu Arg
610 615 620

Leu Asn Gly Arg Gln Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly
625 630 635 640

Leu Lys Ala Ala Tyr Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly
645 650 655

Glu Glu Gln Gln Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe
660 665 670

Phe Val Gly Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser
675 680 685

Ser His Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg
690 695 700

Val Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly
705 710 715 720

Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val Trp
725 730 735

<210> 142

<211> 702

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 142

Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Met Val Glu
1 5 10 15

Tyr Lys Arg Ala Thr Leu Arg Asp Glu Asp Ala Pro Glu Thr Pro Val
20 25 30

Glu Gly Gly Ala Ser Pro Asp Ala Met Glu Val Gly Phe Gln Lys Gly
35 40 45

Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu Glu Leu Val Leu Ala
50 55 60

Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu Leu Gly Cys Leu Val Ala
65 70 75 80

Leu Gly Val Gln Tyr His Arg Asp Pro Ser His Ser Thr Cys Leu Thr
85 90 95

Glu Ala Cys Ile Arg Val Ala Gly Lys Ile Leu Glu Ser Leu Asp Arg
100 105 110

Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys Gly Gly Trp
115 120 125

Ile Arg Arg Asn Pro Leu Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe
 130 135 140
 Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu
 145 150 155 160
 Asn Thr Thr Phe Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg
 165 170 175
 Phe Tyr Leu Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala
 180 185 190
 Gln Pro Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr
 195 200 205
 Gly Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
 210 215 220
 Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala Asp
 225 230 235 240
 Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser Gly Leu
 245 250 255
 Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala Asn Glu Lys
 260 265 270
 Ala Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe Leu Leu
 275 280 285
 Ser Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr Gly Met
 290 295 300
 Asp Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu Pro Ser
 305 310 315 320
 Ile Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr Thr Ser
 325 330 335
 Ser Leu Asp Arg Arg Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr
 340 345 350
 Leu Tyr Gly Thr Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile
 355 360 365
 Ser Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val
 370 375 380
 Lys Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile
 385 390 395 400
 Ser Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp
 405 410 415
 Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala Ile
 420 425 430

Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys Glu Leu
435 440 445

Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser Phe Phe Gln
450 455 460

Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val Met Ala Asp Gln
465 470 475 480

Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser Met Thr Pro Gln Thr
485 490 495

Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn Glu Ile Val Phe Pro Ala
500 505 510

Gly Ile Leu Gln Ala Pro Phe Tyr Ala Arg Asn His Pro Lys Ala Leu
515 520 525

Asn Phe Gly Gly Ile Gly Val Val Met Gly His Glu Leu Thr His Ala
530 535 540

Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Glu Gly Asn Leu Arg Pro
545 550 555 560

Trp Trp Gln Asn Glu Ser Leu Ala Ala Phe Arg Asn His Thr Ala Cys
565 570 575

Met Glu Glu Gln Tyr Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn
580 585 590

Gly Arg Gln Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Lys
595 600 605

Ala Ala Tyr Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu
610 615 620

Gln Gln Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val
625 630 635 640

Gly Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His
645 650 655

Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val Leu
660 665 670

Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly Cys Pro
675 680 685

Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val Trp
690 695 700

<210> 143

<211> 732

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 143

Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Met Val Glu
1 5 10 15

Tyr Lys Arg Ala Thr Leu Arg Asp Glu Asp Ala Pro Glu Thr Pro Val
20 25 30

Glu Gly Gly Ala Ser Pro Asp Ala Met Glu Val Gly Phe Gln Lys Gly
35 40 45

Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu Glu Leu Val Leu Ala
50 55 60

Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu Leu Gly Cys Leu Val Ala
65 70 75 80

Leu Gly Val Gln Tyr His Arg Asp Pro Ser His Ser Thr Cys Leu Thr
85 90 95

Glu Ala Cys Ile Arg Val Ala Gly Lys Ile Leu Glu Ser Leu Asp Arg
100 105 110

Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys Gly Gly Trp
115 120 125

Ile Arg Arg Asn Pro Leu Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe
130 135 140

Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu
145 150 155 160

Asn Thr Thr Phe Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg
165 170 175

Phe Tyr Leu Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala
180 185 190

Gln Pro Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr
195 200 205

Gly Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
210 215 220

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala Asp
225 230 235 240

Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser Gly Leu
245 250 255

Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala Asn Glu Lys
260 265 270

Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu Gly Met Leu Leu
275 280 285

Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met Gln Gln Val Leu Glu
290 295 300

Leu Glu Ile Gln Leu Ala Asn Ile Thr Val Pro Gln Asp Gln Arg Arg
 305 310 315 320
 Asp Glu Glu Lys Ile Tyr His Lys Met Ser Ile Ser Glu Leu Gln Ala
 325 330 335
 Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe Leu Leu Ser
 340 345 350
 Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr Gly Met Asp
 355 360 365
 Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile
 370 375 380
 Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser
 385 390 395 400
 Leu Asp Arg Arg Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu
 405 410 415
 Tyr Gly Thr Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser
 420 425 430
 Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys
 435 440 445
 Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Asp Ala Ile Tyr Asp
 450 455 460
 Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys Glu Leu Asp Asp
 465 470 475 480
 Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser Phe Phe Gln Asn Met
 485 490 495
 Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val Met Ala Asp Gln Leu Arg
 500 505 510
 Lys Pro Pro Ser Arg Asp Gln Trp Ser Met Thr Pro Gln Thr Val Asn
 515 520 525
 Ala Tyr Tyr Leu Pro Thr Lys Asn Glu Ile Val Phe Pro Ala Gly Ile
 530 535 540
 Leu Gln Ala Pro Phe Tyr Ala Arg Asn His Pro Lys Ala Leu Asn Phe
 545 550 555 560
 Gly Gly Ile Gly Val Val Met Gly His Glu Leu Thr His Ala Phe Asp
 565 570 575
 Asp Gln Gly Arg Glu Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp
 580 585 590
 Gln Asn Glu Ser Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu
 595 600 605

Glu Gln Tyr Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg
610 615 620

Gln Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Lys Ala Ala
625 630 635 640

Tyr Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln
645 650 655

Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly Phe
660 665 670

Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His Glu Gly
675 680 685

Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val Leu Gly Thr
690 695 700

Leu Ser Asn Ser Arg Asp Phe Leu Arg His Phe Gly Cys Pro Val Gly
705 710 715 720

Ser Pro Met Asn Pro Gly Gln Leu Cys Glu Val Trp
725 730

<210> 144

<211> 739

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 144

Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Met Val Glu
1 5 10 15

Tyr Lys Arg Ala Thr Leu Arg Asp Glu Asp Ala Pro Glu Thr Pro Val
20 25 30

Glu Gly Gly Ala Ser Pro Asp Ala Met Glu Val Gly Phe Gln Lys Gly
35 40 45

Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu Glu Leu Val Leu Ala
50 55 60

Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu Leu Gly Cys Leu Val Ala
65 70 75 80

Leu Gly Val Gln Tyr His Arg Asp Pro Ser His Ser Thr Cys Leu Thr
85 90 95

Glu Ala Cys Ile Arg Val Ala Gly Lys Ile Leu Glu Ser Leu Asp Arg
100 105 110

Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys Gly Gly Trp
115 120 125

Ile Arg Arg Asn Pro Leu Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe
130 135 140

Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu
145 150 155 160

Asn Thr Thr Phe Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg
165 170 175

Phe Tyr Leu Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala
180 185 190

Gln Pro Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr
195 200 205

Gly Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
210 215 220

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala Asp
225 230 235 240

Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser Gly Leu
245 250 255

Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala Asn Glu Lys
260 265 270

Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu Gly Met Leu Leu
275 280 285

Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met Gln Gln Val Leu Glu
290 295 300

Leu Glu Ile Gln Leu Ala Asn Ile Thr Val Pro Gln Asp Gln Arg Arg
305 310 315 320

Asp Glu Glu Lys Ile Tyr His Lys Met Ser Ile Ser Glu Leu Gln Ala
325 330 335

Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe Leu Leu Ser
340 345 350

Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr Gly Met Asp
355 360 365

Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile
370 375 380

Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser
385 390 395 400

Leu Asp Arg Arg Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu
405 410 415

Tyr Gly Thr Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser
420 425 430

Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys
435 440 445

Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser
450 455 460

Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp Met
465 470 475 480

Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Tyr Glu Ile Ser Glu
485 490 495

Asp Ser Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys
500 505 510

Val Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser
515 520 525

Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn Glu
530 535 540

Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala Arg Asn
545 550 555 560

His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val Met Gly His
565 570 575

Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Glu
580 585 590

Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser Leu Ala Ala Phe Arg
595 600 605

Asn His Thr Ala Cys Met Glu Glu Gln Tyr Asn Gln Tyr Gln Val Asn
610 615 620

Gly Glu Arg Leu Asn Gly Arg Gln Thr Leu Gly Glu Asn Ile Ala Asp
625 630 635 640

Asn Gly Gly Leu Lys Ala Ala Tyr Asn Ala Tyr Lys Ala Trp Leu Arg
645 650 655

Lys His Gly Glu Glu Gln Gln Leu Pro Ala Val Gly Leu Thr Asn His
660 665 670

Gln Leu Phe Phe Val Gly Phe Ala Gln Val Trp Cys Ser Val Arg Thr
675 680 685

Pro Glu Ser Ser His Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala
690 695 700

Arg Phe Arg Val Leu Gly Thr Leu Ser Asn Ser Arg Asp Phe Leu Arg
705 710 715 720

His Phe Gly Cys Pro Val Gly Ser Pro Met Asn Pro Gly Gln Leu Cys
725 730 735

Glu Val Trp

<210> 145

<211> 728

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 145

Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Met Val Glu
1 5 10 15

Tyr Lys Arg Ala Thr Leu Arg Asp Glu Asp Ala Pro Glu Thr Pro Val
20 25 30

Glu Gly Gly Ala Ser Pro Asp Ala Met Glu Val Gly Phe Gln Lys Gly
35 40 45

Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu Glu Leu Val Leu Ala
50 55 60

Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu Leu Gly Cys Leu Val Ala
65 70 75 80

Leu Gly Val Gln Tyr His Arg Asp Pro Ser His Ser Thr Cys Leu Thr
85 90 95

Glu Ala Cys Ile Arg Val Ala Gly Lys Ile Leu Glu Ser Leu Asp Arg
100 105 110

Gly Val Ser Pro Cys Glu Asp Phe Tyr Gln Phe Ser Cys Gly Gly Trp
115 120 125

Ile Arg Arg Asn Pro Leu Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe
130 135 140

Asn Ser Leu Trp Asp Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu
145 150 155 160

Asn Thr Thr Phe Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg
165 170 175

Phe Tyr Leu Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala
180 185 190

Gln Pro Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr
195 200 205

Gly Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala
210 215 220

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala Asp
225 230 235 240

Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser Gly Leu
245 250 255

Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala Asn Glu Lys
260 265 270

Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu Gly Met Leu Leu
 275 280 285
 Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met Gln Gln Val Leu Glu
 290 295 300
 Leu Glu Ile Gln Leu Ala Asn Ile Thr Val Pro Gln Asp Gln Arg Arg
 305 310 315 320
 Asp Glu Glu Lys Ile Tyr His Lys Met Ser Ile Ser Glu Leu Gln Ala
 325 330 335
 Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe Leu Leu Ser
 340 345 350
 Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr Gly Met Asp
 355 360 365
 Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile
 370 375 380
 Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser
 385 390 395 400
 Leu Asp Arg Arg Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu
 405 410 415
 Tyr Gly Thr Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser
 420 425 430
 Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys
 435 440 445
 Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser
 450 455 460
 Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp Met
 465 470 475 480
 Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala Ile Tyr
 485 490 495
 Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys Glu Leu Asp
 500 505 510
 Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser Phe Phe Gln Asn
 515 520 525
 Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val Met Ala Asp Gln Leu
 530 535 540
 Arg Lys Pro Pro Ser Arg Asp Gln Ala Leu Asn Phe Gly Gly Ile Gly
 545 550 555 560
 Val Val Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg
 565 570 575
 Glu Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser

580 585 590
 Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr Asn
 595 600 605
 Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg Gln Thr Leu Gly
 610 615 620
 Glu Asn Ile Ala Asp Asn Gly Gly Leu Lys Ala Ala Tyr Asn Ala Tyr
 625 630 635 640
 Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln Leu Pro Ala Val
 645 650 655
 Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly Phe Ala Gln Val Trp
 660 665 670
 Cys Ser Val Arg Thr Pro Glu Ser Ser His Glu Gly Leu Val Thr Asp
 675 680 685
 Pro His Ser Pro Ala Arg Phe Arg Val Leu Gly Thr Leu Ser Asn Ser
 690 695 700
 Arg Asp Phe Leu Arg His Phe Gly Cys Pro Val Gly Ser Pro Met Asn
 705 710 715 720
 Pro Gly Gln Leu Cys Glu Val Trp
 725
 <210> 146
 <211> 117
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 146
 Met Ala Arg Ala Leu Cys Pro Leu Gln Ala Leu Trp Leu Leu Glu Trp
 1 5 10 15
 Val Leu Leu Leu Leu Gly Pro Cys Ala Ala Pro Pro Ala Trp Ala Leu
 20 25 30
 Asn Leu Asp Pro Val Gln Leu Thr Phe Tyr Ala Gly Pro Asn Gly Ser
 35 40 45
 Gln Phe Gly Phe Ser Leu Asp Phe His Lys Asp Ser His Gly Arg Val
 50 55 60
 Ala Ile Val Val Gly Ala Pro Arg Thr Leu Gly Pro Ser Gln Glu Glu
 65 70 75 80
 Thr Gly Gly Val Phe Leu Cys Pro Trp Arg Ala Glu Gly Gly Gln Cys
 85 90 95
 Pro Ser Leu Leu Phe Asp Leu Arg Leu Arg Pro Leu Ala Ala Leu Glu
 100 105 110

Arg Pro Arg Lys Asp
115

<210> 147
<211> 34
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 147

Met Pro Ser Trp Ala Leu Phe Met Val Thr Ser Cys Leu Leu Leu Ala
1 5 10 15

Pro Gln Asn Leu Ala Gln Val Ser Ser Gln Gly Arg Ser Pro Val Leu
20 25 30

Ala Pro

<210> 148
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 148

Met Ala Thr Ser Asn Leu Leu Lys Gly Cys Ala Cys Ser Leu Ser Leu
1 5 10 15

Gly

<210> 149
<211> 662
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 149

Met Gly Lys Gln Gly Ser Asn Lys Lys Ser Asn Val Glu Asp Ser Ile
1 5 10 15

Val Arg Lys Leu Met Leu Asp Thr Trp Asn Glu Ser Ile Phe Ser Asn
20 25 30

Ile Lys Asn Arg Leu Gln Asp Ser Ala Met Lys Leu Val His Ala Glu
35 40 45

Arg Leu Gly Glu Ala Phe Asp Ser Gln Leu Val Ile Gly Val Arg Glu
50 55 60

Ser Tyr Val Asn Leu Cys Ser Asn Pro Glu Asp Lys Leu Gln Ile Tyr
65 70 75 80

Arg Asp Asn Phe Glu Lys Ala Tyr Leu Asp Ser Thr Glu Arg Phe Tyr
85 90 95

Arg Thr Gln Ala Pro Ser Tyr Leu Gln Gln Asn Gly Val Gln Asn Tyr
 100 105 110
 Met Lys Tyr Ala Asp Ala Lys Leu Lys Glu Glu Glu Lys Arg Ala Leu
 115 120 125
 Arg Tyr Leu Glu Thr Arg Arg Glu Cys Asn Ser Val Glu Ala Leu Met
 130 135 140
 Glu Cys Cys Val Asn Ala Leu Val Thr Ser Phe Lys Glu Thr Ile Leu
 145 150 155 160
 Ala Glu Cys Gln Gly Met Ile Lys Arg Asn Glu Thr Glu Lys Leu His
 165 170 175
 Leu Met Phe Ser Leu Met Asp Lys Val Pro Asn Gly Ile Glu Pro Met
 180 185 190
 Leu Lys Asp Leu Glu Glu His Ile Ile Ser Ala Gly Leu Ala Asp Met
 195 200 205
 Val Ala Ala Ala Glu Thr Ile Thr Thr Asp Ser Glu Lys Tyr Val Glu
 210 215 220
 Gln Leu Leu Thr Leu Phe Asn Arg Phe Ser Lys Leu Val Lys Glu Ala
 225 230 235 240
 Phe Gln Asp Asp Pro Arg Phe Leu Thr Ala Arg Asp Lys Ala Tyr Lys
 245 250 255
 Ala Val Val Asn Asp Ala Thr Ile Phe Lys Leu Glu Leu Pro Leu Lys
 260 265 270
 Gln Lys Gly Val Gly Leu Lys Thr Gln Pro Glu Ser Lys Cys Pro Glu
 275 280 285
 Leu Leu Ala Asn Tyr Cys Asp Met Leu Leu Arg Lys Thr Pro Leu Ser
 290 295 300
 Lys Lys Leu Thr Ser Glu Glu Ile Glu Ala Lys Leu Lys Glu Val Leu
 305 310 315 320
 Leu Val Leu Lys Tyr Val Gln Asn Lys Asp Val Phe Met Arg Tyr His
 325 330 335
 Lys Ala His Leu Thr Arg Arg Leu Ile Leu Asp Ile Ser Ala Asp Ser
 340 345 350
 Glu Ile Glu Glu Asn Met Val Glu Trp Leu Arg Glu Val Gly Met Pro
 355 360 365
 Ala Asp Tyr Val Asn Lys Leu Ala Arg Met Phe Gln Asp Ile Lys Val
 370 375 380
 Ser Glu Asp Leu Asn Gln Ala Phe Lys Glu Met His Lys Asn Asn Lys
 385 390 395 400

Leu Ala Leu Pro Ala Asp Ser Val Asn Ile Lys Ile Leu Asn Ala Gly
405 410 415

Ala Trp Ser Arg Ser Ser Glu Lys Val Phe Val Ser Leu Pro Thr Glu
420 425 430

Leu Glu Asp Leu Ile Pro Glu Val Glu Glu Phe Tyr Lys Lys Asn His
435 440 445

Ser Gly Arg Lys Leu His Trp His His Leu Met Ser Asn Gly Ile Ile
450 455 460

Thr Phe Lys Asn Glu Val Gly Gln Tyr Asp Leu Glu Val Thr Thr Phe
465 470 475 480

Gln Leu Ala Val Leu Phe Ala Trp Asn Gln Arg Pro Arg Glu Lys Ile
485 490 495

Ser Phe Glu Asn Leu Lys Leu Ala Thr Glu Leu Pro Asp Ala Glu Leu
500 505 510

Arg Arg Thr Leu Trp Ser Leu Val Ala Phe Pro Lys Leu Lys Arg Gln
515 520 525

Val Leu Leu Tyr Glu Pro Gln Val Asn Ser Pro Lys Asp Phe Thr Glu
530 535 540

Gly Thr Leu Phe Ser Val Asn Gln Glu Phe Ser Leu Ile Lys Asn Ala
545 550 555 560

Lys Val Gln Lys Arg Gly Lys Ile Asn Leu Ile Gly Arg Leu Gln Leu
565 570 575

Thr Thr Glu Arg Met Arg Glu Glu Glu Asn Glu Gly Ile Val Gln Leu
580 585 590

Arg Ile Leu Arg Thr Gln Glu Ala Ile Ile Gln Ile Met Lys Met Arg
595 600 605

Lys Lys Ile Ser Asn Ala Gln Leu Gln Thr Glu Leu Val Glu Ile Leu
610 615 620

Lys Asn Met Phe Leu Pro Gln Lys Lys Met Ile Lys Glu Gln Ile Glu
625 630 635 640

Trp Leu Ile Glu His Lys Tyr Ile Arg Arg Asp Glu Ser Asp Ile Asn
645 650 655

Thr Phe Ile Tyr Met Ala
660

<210> 150

<211> 263

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 150

Met Ala Thr Ser Asn Leu Leu Lys Asn Lys Gly Ser Leu Gln Phe Glu
1 5 10 15

Asp Lys Trp Asp Phe Met Arg Pro Ile Val Leu Lys Leu Leu Arg Gln
20 25 30

Glu Ser Val Thr Lys Gln Gln Trp Phe Asp Leu Phe Ser Asp Val His
35 40 45

Ala Val Cys Leu Trp Asp Asp Lys Gly Pro Ala Lys Ile His Gln Ala
50 55 60

Leu Lys Glu Asp Ile Leu Glu Phe Ile Lys Gln Ala Gln Ala Arg Val
65 70 75 80

Leu Ser His Gln Asp Asp Thr Ala Leu Leu Lys Ala Tyr Ile Val Glu
85 90 95

Trp Arg Lys Phe Phe Thr Gln Cys Asp Ile Leu Pro Lys Pro Phe Cys
100 105 110

Gln Leu Glu Ile Thr Leu Met Gly Lys Gln Gly Ser Asn Lys Lys Ser
115 120 125

Asn Val Glu Asp Ser Ile Val Arg Lys Leu Met Leu Asp Thr Trp Asn
130 135 140

Glu Ser Ile Phe Ser Asn Ile Lys Asn Arg Leu Gln Asp Ser Ala Met
145 150 155 160

Lys Leu Val His Ala Glu Arg Leu Gly Glu Ala Phe Asp Ser Gln Leu
165 170 175

Val Ile Gly Val Arg Glu Ser Tyr Val Asn Leu Cys Ser Asn Pro Glu
180 185 190

Asp Lys Leu Gln Ile Tyr Arg Asp Asn Phe Glu Lys Ala Tyr Leu Asp
195 200 205

Ser Thr Glu Arg Phe Tyr Arg Thr Gln Ala Pro Ser Tyr Leu Gln Gln
210 215 220

Asn Gly Val Gln Asn Tyr Met Lys Tyr Ala Asp Ala Lys Leu Lys Glu
225 230 235 240

Glu Glu Lys Arg Ala Leu Arg Tyr Leu Glu Thr Arg Arg Glu Cys Asn
245 250 255

Ser Val Glu Ala Asn Tyr Ile
260

<210> 151

<211> 380

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 151

Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
1 5 10 15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
225 230 235 240

Gln Leu Gly Glu Asp Phe Ile Gln Leu His Lys Leu Leu Arg Lys Ser
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Ile Ile Gly Tyr
355 360 365

Leu Phe Cys Ser Arg Asn Trp Trp Ala Pro Arg Cys
370 375 380

<210> 152

<211> 263

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 152

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
85 90 95

Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
100 105 110

Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
115 120 125

Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
130 135 140

Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
145 150 155 160

Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
165 170 175

Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
180 185 190

Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
195 200 205

Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
210 215 220

Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
225 230 235 240

Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
245 250 255

Trp Glu Leu Gly Asn Asp Ser
260

<210> 153

<211> 577

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 153

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
85 90 95

Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
100 105 110

Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
115 120 125

Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
130 135 140

Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
145 150 155 160

Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
165 170 175

Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln

180 185 190
 Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
 195 200 205
 Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
 210 215 220
 Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
 225 230 235 240
 Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
 245 250 255
 Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
 260 265 270
 Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
 275 280 285
 Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
 290 295 300
 Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly His
 305 310 315 320
 Cys Tyr Ile Asp Gly Arg Val Val Lys Val Met Asp Phe Leu Lys Thr
 325 330 335
 Arg Leu Leu Asp Thr Leu Ser Asp Gln Ile Arg Lys Ile Gln Lys Val
 340 345 350
 Val Asn Thr Tyr Thr Pro Gly Lys Lys Ile Trp Leu Glu Gly Val Val
 355 360 365
 Thr Thr Ser Ala Gly Gly Thr Asn Asn Leu Ser Asp Ser Tyr Ala Ala
 370 375 380
 Gly Phe Leu Trp Leu Asn Thr Leu Gly Met Leu Ala Asn Gln Gly Ile
 385 390 395 400
 Asp Val Val Ile Arg His Ser Phe Phe Asp His Gly Tyr Asn His Leu
 405 410 415
 Val Asp Gln Asn Phe Asn Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu
 420 425 430
 Tyr Lys Arg Leu Ile Gly Pro Lys Val Leu Ala Val His Val Ala Gly
 435 440 445
 Leu Gln Arg Lys Pro Arg Pro Gly Arg Val Ile Arg Asp Lys Leu Arg
 450 455 460
 Ile Tyr Ala His Cys Thr Asn His His Asn His Asn Tyr Val Arg Gly
 465 470 475 480
 Ser Ile Thr Leu Phe Ile Ile Asn Leu His Arg Ser Arg Lys Lys Ile
 485 490 495

Lys Leu Ala Gly Thr Leu Arg Asp Lys Leu Val His Gln Tyr Leu Leu
500 505 510

Gln Pro Tyr Gly Gln Glu Gly Leu Lys Ser Lys Ser Val Gln Leu Asn
515 520 525

Gly Gln Pro Leu Val Met Val Asp Asp Gly Thr Leu Pro Glu Leu Lys
530 535 540

Pro Arg Pro Leu Arg Ala Gly Arg Thr Leu Val Ile Pro Pro Val Thr
545 550 555 560

Met Gly Phe Phe Val Val Lys Asn Val Asn Ala Leu Ala Cys Arg Tyr
565 570 575

Arg

<210> 154

<211> 351

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 154

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
85 90 95

Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
100 105 110

Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
115 120 125

Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
130 135 140

Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
145 150 155 160

Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu

165 170 175
 Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
 180 185 190
 Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
 195 200 205
 Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
 210 215 220
 Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
 225 230 235 240
 Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
 245 250 255
 Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
 260 265 270
 Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
 275 280 285
 Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
 290 295 300
 Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly Phe
 305 310 315 320
 Met Lys Val Ala Gly Ser Thr Val Asp Ala Val Thr Trp Gln Gln Trp
 325 330 335
 Leu Ile His Thr Leu Gln Glu Arg Arg Phe Gly Leu Lys Val Trp
 340 345 350

<210> 155

<211> 379

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 155

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
 1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
 20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
 35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
 50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
 65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
 85 90 95
 Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
 100 105 110
 Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
 115 120 125
 Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
 130 135 140
 Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
 145 150 155 160
 Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
 165 170 175
 Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
 180 185 190
 Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
 195 200 205
 Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
 210 215 220
 Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
 225 230 235 240
 Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
 245 250 255
 Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
 260 265 270
 Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
 275 280 285
 Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
 290 295 300
 Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly Phe
 305 310 315 320
 Met Lys Val Ala Gly Ser Thr Val Asp Ala Val Thr Trp Gln His Cys
 325 330 335
 Tyr Ile Asp Gly Arg Val Val Lys Val Met Asp Phe Leu Lys Thr Arg
 340 345 350
 Leu Leu Asp Thr Leu Ser Asp Gln Ile Arg Lys Ile Gln Lys Met Val
 355 360 365
 Glu His Phe Arg Ile Ala Gly Gln Ser Gly His
 370 375

<210> 156

<211> 411
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> A novel predicted alternative spliced variant protein product

 <400> 156

 Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
 1 5 10 15

 Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
 20 25 30

 Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
 35 40 45

 Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
 50 55 60

 Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
 65 70 75 80

 Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
 85 90 95

 Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
 100 105 110

 Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
 115 120 125

 Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
 130 135 140

 Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
 145 150 155 160

 Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
 165 170 175

 Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
 180 185 190

 Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
 195 200 205

 Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
 210 215 220

 Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
 225 230 235 240

 Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
 245 250 255

 Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
 260 265 270

Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
275 280 285

Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
290 295 300

Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly Phe
305 310 315 320

Met Lys Val Ala Gly Ser Thr Val Asp Ala Val Thr Trp Gln His Cys
325 330 335

Tyr Ile Asp Gly Arg Val Val Lys Val Met Asp Phe Leu Lys Thr Arg
340 345 350

Leu Leu Asp Thr Leu Ser Asp Gln Ile Arg Lys Ile Gln Lys Val Val
355 360 365

Asn Thr Tyr Thr Pro Gly Lys Lys Ile Trp Leu Glu Gly Val Val Thr
370 375 380

Thr Ser Ala Gly Gly Thr Asn Asn Leu Ser Asp Ser Tyr Ala Ala Gly
385 390 395 400

Phe Thr Thr Gly Ser Leu Ser Ser Thr Ser Ala
405 410

<210> 157

<211> 565

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 157

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
85 90 95

Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
100 105 110

Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
115 120 125

Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
 130 135 140
 Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
 145 150 155 160
 Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
 165 170 175
 Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
 180 185 190
 Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
 195 200 205
 Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
 210 215 220
 Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
 225 230 235 240
 Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
 245 250 255
 Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
 260 265 270
 Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
 275 280 285
 Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
 290 295 300
 Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly Phe
 305 310 315 320
 Met Lys Val Ala Gly Ser Thr Val Asp Ala Val Thr Trp Gln His Cys
 325 330 335
 Tyr Ile Asp Gly Arg Val Val Lys Val Met Asp Phe Leu Lys Thr Arg
 340 345 350
 Leu Leu Asp Thr Leu Ser Asp Gln Ile Arg Lys Ile Gln Lys Val Val
 355 360 365
 Asn Thr Tyr Thr Pro Gly Lys Lys Ile Trp Leu Glu Gly Val Val Thr
 370 375 380
 Thr Ser Ala Gly Gly Thr Asn Asn Leu Ser Asp Ser Tyr Ala Ala Gly
 385 390 395 400
 Phe Leu Trp Leu Asn Thr Leu Gly Met Leu Ala Asn Gln Gly Ile Asp
 405 410 415
 Val Val Ile Arg His Ser Phe Phe Asp His Gly Tyr Asn His Leu Val
 420 425 430

Asp Gln Asn Phe Asn Pro Leu Pro Pro Gln Leu Arg Ser Trp Val His
435 440 445

Tyr Thr Phe Tyr His Gln Leu Ala Ser Ile Lys Lys Glu Asn Gln Ala
450 455 460

Gly Trp Asp Ser Gln Arg Gln Ala Gly Ser Pro Val Pro Ala Ala Ala
465 470 475 480

Leu Trp Ala Gly Gly Pro Lys Val Gln Val Ser Ala Thr Glu Trp Pro
485 490 495

Ala Leu Ser Asp Gly Gly Arg Arg Asp Pro Pro Arg Ile Glu Ala Pro
500 505 510

Pro Pro Ser Gly Arg Pro Asp Ile Gly His Pro Ser Ser His His Gly
515 520 525

Leu Leu Cys Gly Gln Glu Cys Gln Cys Phe Gly Leu Pro Leu Pro Ile
530 535 540

Ser Tyr Pro His Thr His Gly Tyr Gln Trp Ala Cys Trp Ala Ala Ser
545 550 555 560

Thr Pro Pro Leu Gln
565

<210> 158

<211> 544

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 158

Met Arg Val Leu Cys Ala Phe Pro Glu Ala Met Pro Ser Ser Asn Ser
1 5 10 15

Arg Pro Pro Ala Cys Leu Ala Pro Gly Ala Leu Tyr Leu Ala Leu Leu
20 25 30

Leu His Leu Ser Leu Ser Ser Gln Ala Gly Asp Arg Arg Pro Leu Pro
35 40 45

Val Asp Arg Ala Ala Gly Leu Lys Glu Lys Thr Leu Ile Leu Leu Asp
50 55 60

Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
65 70 75 80

Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
85 90 95

Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe
100 105 110

Leu Arg Phe Gly Gly Lys Arg Thr Asp Phe Leu Gln Phe Gln Asn Leu
115 120 125

Arg Asn Pro Ala Lys Ser Arg Gly Gly Pro Gly Pro Asp Tyr Tyr Leu
130 135 140

Lys Asn Tyr Glu Asp Asp Ile Val Arg Ser Asp Val Ala Leu Asp Lys
145 150 155 160

Gln Lys Gly Cys Lys Ile Ala Gln His Pro Asp Val Met Leu Glu Leu
165 170 175

Gln Arg Glu Lys Ala Ala Gln Met His Leu Val Leu Leu Lys Glu Gln
180 185 190

Phe Ser Asn Thr Tyr Ser Asn Leu Ile Leu Thr Ala Arg Ser Leu Asp
195 200 205

Lys Leu Tyr Asn Phe Ala Asp Cys Ser Gly Leu His Leu Ile Phe Ala
210 215 220

Leu Asn Ala Leu Arg Arg Asn Pro Asn Asn Ser Trp Asn Ser Ser Ser
225 230 235 240

Ala Leu Ser Leu Leu Lys Tyr Ser Ala Ser Lys Lys Tyr Asn Ile Ser
245 250 255

Trp Glu Leu Gly Asn Glu Pro Asn Asn Tyr Arg Thr Met His Gly Arg
260 265 270

Ala Val Asn Gly Ser Gln Leu Gly Lys Asp Tyr Ile Gln Leu Lys Ser
275 280 285

Leu Leu Gln Pro Ile Arg Ile Tyr Ser Arg Ala Ser Leu Tyr Gly Pro
290 295 300

Asn Ile Gly Arg Pro Arg Lys Asn Val Ile Ala Leu Leu Asp Gly Phe
305 310 315 320

Met Lys Val Ala Gly Ser Thr Val Asp Ala Val Thr Trp Gln His Cys
325 330 335

Tyr Ile Asp Gly Arg Val Val Lys Val Met Asp Phe Leu Lys Thr Arg
340 345 350

Leu Leu Asp Thr Leu Ser Asp Gln Ile Arg Lys Ile Gln Lys Val Val
355 360 365

Asn Thr Tyr Thr Pro Gly Lys Lys Ile Trp Leu Glu Gly Val Val Thr
370 375 380

Thr Ser Ala Gly Gly Thr Asn Asn Leu Ser Asp Ser Tyr Ala Ala Gly
385 390 395 400

Phe Leu Trp Leu Asn Thr Leu Gly Met Leu Ala Asn Gln Gly Ile Asp
405 410 415

Val Val Ile Arg His Ser Phe Phe Asp His Gly Tyr Asn His Leu Val
420 425 430

Asp Gln Asn Phe Asn Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Tyr
435 440 445

Lys Arg Leu Ile Gly Pro Lys Val Leu Ala Val His Val Ala Gly Leu
450 455 460

Gln Arg Lys Pro Arg Pro Gly Arg Val Ile Arg Asp Lys Leu Arg Ile
465 470 475 480

Tyr Ala His Cys Thr Asn His His Asn Lys Ser Val Gln Leu Asn Gly
485 490 495

Gln Pro Leu Val Met Val Asp Asp Gly Thr Leu Pro Glu Leu Lys Pro
500 505 510

Arg Pro Leu Arg Ala Gly Arg Thr Leu Val Ile Pro Pro Val Thr Met
515 520 525

Gly Phe Phe Val Val Lys Asn Val Asn Ala Leu Ala Cys Arg Tyr Arg
530 535 540

<210> 159
<211> 695
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 159

Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys
1 5 10 15

Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val
20 25 30

Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr
35 40 45

Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser
50 55 60

Asp Val Leu Gln Glu Pro Lys Thr Glu Asp Ile Val Ala Val Gln Lys
65 70 75 80

Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn Glu Ser Ala Ile Asp Ser
85 90 95

Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu Pro Asp Ile Tyr Gly Trp
100 105 110

Pro Val Ala Thr Glu Asn Trp Glu Gln Lys Tyr Gly Ala Ser Trp Thr
115 120 125

Ala Glu Lys Ala Ile Ala Gln Leu Asn Ser Lys Tyr Gly Lys Lys Val
130 135 140

Leu Ile Asn Leu Phe Val Gly Thr Asp Asp Lys Asn Ser Val Asn His
145 150 155 160

Val Ile His Ile Asp Gln Pro Arg Leu Gly Leu Pro Ser Arg Asp Tyr
165 170 175

Tyr Glu Cys Thr Gly Ile Tyr Lys Glu Ala Cys Thr Ala Tyr Val Asp
180 185 190

Phe Met Ile Ser Val Ala Arg Leu Ile Arg Gln Glu Glu Arg Leu Pro
195 200 205

Ile Asp Glu Asn Gln Leu Ala Leu Glu Met Asn Lys Val Met Glu Leu
210 215 220

Glu Lys Glu Ile Ala Asn Ala Thr Ala Lys Pro Glu Asp Arg Asn Asp
225 230 235 240

Pro Met Leu Leu Tyr Asn Lys Met Thr Leu Ala Gln Ile Gln Asn Asn
245 250 255

Phe Ser Leu Glu Ile Asn Gly Lys Pro Phe Ser Trp Leu Asn Phe Thr
260 265 270

Asn Glu Ile Met Ser Thr Val Asn Ile Ser Ile Thr Asn Glu Glu Asp
275 280 285

Val Val Val Tyr Ala Pro Glu Tyr Leu Thr Lys Leu Lys Pro Ile Leu
290 295 300

Thr Lys Tyr Ser Ala Arg Asp Leu Gln Asn Leu Met Ser Trp Arg Phe
305 310 315 320

Ile Met Asp Leu Val Ser Ser Leu Ser Arg Thr Tyr Lys Glu Ser Arg
325 330 335

Asn Ala Phe Arg Lys Ala Leu Tyr Gly Thr Thr Ser Glu Thr Ala Thr
340 345 350

Trp Arg Arg Cys Ala Asn Tyr Val Asn Gly Asn Met Glu Asn Ala Val
355 360 365

Gly Arg Leu Tyr Val Glu Ala Ala Phe Ala Gly Glu Ser Lys His Val
370 375 380

Val Glu Asp Leu Ile Ala Gln Ile Arg Glu Val Phe Ile Gln Thr Leu
385 390 395 400

Asp Asp Leu Thr Trp Met Asp Ala Glu Thr Lys Lys Arg Ala Glu Glu
405 410 415

Lys Ala Leu Ala Ile Lys Glu Arg Ile Gly Tyr Pro Asp Asp Ile Val
420 425 430

Ser Asn Asp Asn Lys Leu Asn Asn Glu Tyr Leu Glu Leu Asn Tyr Lys
435 440 445

Glu Asp Glu Tyr Phe Glu Asn Ile Ile Gln Asn Leu Lys Phe Ser Gln
450 455 460

Ser Lys Gln Leu Lys Lys Leu Arg Glu Lys Val Asp Lys Asp Glu Trp
465 470 475 480

Ile Ser Gly Ala Ala Val Val Asn Ala Phe Tyr Ser Ser Gly Arg Asn
485 490 495

Gln Ile Val Phe Pro Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Ala
500 505 510

Gln Gln Ser Asn Ser Leu Asn Tyr Gly Gly Ile Gly Met Val Ile Gly
515 520 525

His Glu Ile Thr His Gly Phe Asp Asp Asn Gly Arg Asn Phe Asn Lys
530 535 540

Asp Gly Asp Leu Val Asp Trp Trp Thr Gln Gln Ser Ala Ser Asn Phe
545 550 555 560

Lys Glu Gln Ser Gln Cys Met Val Tyr Gln Tyr Gly Asn Phe Ser Trp
565 570 575

Asp Leu Ala Gly Gly Gln His Leu Asn Gly Ile Asn Thr Leu Gly Glu
580 585 590

Asn Ile Ala Asp Asn Gly Gly Leu Gly Gln Ala Tyr Arg Ala Tyr Gln
595 600 605

Asn Tyr Ile Lys Lys Asn Gly Glu Glu Lys Leu Leu Pro Gly Leu Asp
610 615 620

Leu Asn His Lys Gln Leu Phe Phe Leu Asn Phe Ala Gln Val Trp Cys
625 630 635 640

Gly Thr Tyr Arg Pro Glu Tyr Ala Val Asn Ser Ile Lys Thr Asp Val
645 650 655

His Ser Pro Gly Asn Phe Arg Ile Ile Gly Thr Leu Gln Asn Ser Ala
660 665 670

Glu Phe Ser Glu Ala Phe His Cys Arg Lys Asn Ser Tyr Met Asn Pro
675 680 685

Glu Lys Lys Cys Arg Val Trp
690 695

<210> 160
<211> 178
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 160

Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys
1 5 10 15

Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val
20 25 30

Leu Val Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr
35 40 45

Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser
50 55 60

Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys Thr
65 70 75 80

Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val Ile
85 90 95

Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp Glu
100 105 110

Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu Asp
115 120 125

Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn
130 135 140

Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu
145 150 155 160

Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln Lys
165 170 175

Tyr Asp

<210> 161

<211> 704

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 161

Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys
1 5 10 15

Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val
20 25 30

Leu Val Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr
35 40 45

Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser
50 55 60

Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys Thr
65 70 75 80

Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val Ile
85 90 95

Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp Glu
100 105 110

Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu Asp
 115 120 125
 Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn
 130 135 140
 Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu
 145 150 155 160
 Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln Lys
 165 170 175
 Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn Ser
 180 185 190
 Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp Asp
 195 200 205
 Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu Gly
 210 215 220
 Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu Ala
 225 230 235 240
 Thr Ala Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys
 245 250 255
 Met Thr Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly
 260 265 270
 Lys Pro Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val
 275 280 285
 Asn Ile Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu
 290 295 300
 Tyr Leu Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp
 305 310 315 320
 Leu Gln Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser
 325 330 335
 Leu Ser Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu
 340 345 350
 Tyr Gly Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr
 355 360 365
 Val Asn Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala
 370 375 380
 Ala Phe Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln
 385 390 395 400
 Ile Arg Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp
 405 410 415

Ala Glu Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu
420 425 430

Arg Ile Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn
435 440 445

Asn Glu Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn
450 455 460

Ile Ile Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu
465 470 475 480

Arg Glu Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val
485 490 495

Asn Ala Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly
500 505 510

Ile Leu Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn
515 520 525

Tyr Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe
530 535 540

Asp Asp Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp
545 550 555 560

Trp Thr Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met
565 570 575

Val Tyr Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His
580 585 590

Leu Asn Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly
595 600 605

Leu Gly Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly
610 615 620

Glu Glu Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe
625 630 635 640

Phe Leu Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr
645 650 655

Ala Val Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg
660 665 670

Ile Ile Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His
675 680 685

Cys Arg Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
690 695 700

<210> 162

<211> 389

<212> PRT

<213> Artificial sequence

<220>

<223> A novel, predicted alternative spliced variant protein product

<400> 162

Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys
 1 5 10 15

Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val
 20 25 30

Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr
 35 40 45

Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser
 50 55 60

Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys Thr
 65 70 75 80

Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val Ile
 85 90 95

Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp Glu
 100 105 110

Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu Asp
 115 120 125

Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn
 130 135 140

Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu
 145 150 155 160

Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln Lys
 165 170 175

Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn Ser
 180 185 190

Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp Asp
 195 200 205

Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu Gly
 210 215 220

Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu Ala
 225 230 235 240

Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile Arg
 245 250 255

Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu Met
 260 265 270

Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala Lys
 275 280 285

Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr Leu
290 295 300

Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Arg Ser
305 310 315 320

Ser Lys Phe Asn Val Leu Glu Ile His Asn Gly Ser Cys Lys Gln Pro
325 330 335

Gln Pro Asn Leu Gln Gly Val Gln Lys Cys Phe Pro Gln Gly Pro Leu
340 345 350

Trp Tyr Asn Leu Arg Asn Ser Asn Leu Glu Thr Leu Cys Lys Leu Cys
355 360 365

Gln Trp Glu Tyr Gly Lys Cys Cys Gly Glu Ala Leu Cys Gly Ser Ser
370 375 380

Ile Cys Trp Arg Glu
385

<210> 163

<211> 410

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 163

Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys
1 5 10 15

Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val
20 25 30

Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr
35 40 45

Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser
50 55 60

Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys Thr
65 70 75 80

Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val Ile
85 90 95

Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp Glu
100 105 110

Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu Asp
115 120 125

Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn
130 135 140

Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu
145 150 155 160

Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln Lys
 165 170 175
 Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn Ser
 180 185 190
 Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp Asp
 195 200 205
 Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu Gly
 210 215 220
 Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu Ala
 225 230 235 240
 Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile Arg
 245 250 255
 Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu Met
 260 265 270
 Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala Lys
 275 280 285
 Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr Leu
 290 295 300
 Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro Phe
 305 310 315 320
 Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile Ser
 325 330 335
 Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu Thr
 340 345 350
 Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Pro Phe Met Val
 355 360 365
 Gln Pro Gln Lys Gln Gln Leu Gly Asp Val Val Gln Thr Met Ser Met
 370 375 380
 Gly Ile Trp Lys Met Leu Trp Gly Gly Phe Met Trp Lys Gln His Leu
 385 390 395 400
 Leu Glu Arg Val Asn Met Trp Ser Arg Ile
 405 410
 <210> 164
 <211> 529
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 164
 Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro Lys

1	5	10	15
Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser Val	20	25	30
Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu Tyr	35	40	45
Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys Ser	50	55	60
Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys Thr	65	70	75
Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val Ile	85	90	95
Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp Glu	100	105	110
Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu Asp	115	120	125
Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile Asn	130	135	140
Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu Leu	145	150	155
Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln Lys	165	170	175
Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn Ser	180	185	190
Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp Asp	195	200	205
Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu Gly	210	215	220
Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu Ala	225	230	235
Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile Arg	245	250	255
Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu Met	260	265	270
Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala Lys	275	280	285
Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr Leu	290	295	300
Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro Phe	305	310	315

Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile Ser
 325 330 335
 Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu Thr
 340 345 350
 Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln Asn
 355 360 365
 Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser Arg
 370 375 380
 Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly Thr
 385 390 395 400
 Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn Gly
 405 410 415
 Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe Ala
 420 425 430
 Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg Glu
 435 440 445
 Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu Thr
 450 455 460
 Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile Gly
 465 470 475 480
 Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu Tyr
 485 490 495
 Leu Glu Val Asp Lys Trp Ser Ser Cys Ser Gln Cys Ile Leu Leu Phe
 500 505 510
 Arg Lys Lys Ser Asp Ser Leu Pro Ser Arg His Ser Ala Ala Pro Leu
 515 520 525
 Leu
 <210> 165
 <211> 252
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> A novel predicted alternative spliced variant protein product
 <400> 165
 Met Ser Val Pro Ser Ser Leu Ser Gln Ser Ala Ile Asn Ala Asn Ser
 1 5 10 15
 His Gly Gly Pro Ala Leu Ser Leu Pro Leu Pro Leu His Ala Ala His
 20 25 30
 Asn Gln Leu Leu Asn Ala Lys Leu Gln Ala Thr Ala Val Gly Pro Lys

35 40 45
 Asp Leu Arg Ser Ala Met Gly Glu Gly Gly Gly Pro Glu Pro Gly Pro
 50 55 60
 Ala Asn Ala Lys Trp Leu Lys Glu Gly Gln Asn Gln Leu Arg Arg Ala
 65 70 75 80
 Ala Thr Ala His Arg Asp Gln Asn Arg Asn Val Thr Leu Thr Leu Ala
 85 90 95
 Glu Glu Ala Ser Gln Glu Pro Glu Met Ala Pro Leu Gly Pro Lys Gly
 100 105 110
 Leu Ile His Leu Tyr Ser Glu Leu Glu Leu Ser Ala His Asn Ala Ala
 115 120 125
 Asn Arg Gly Leu Arg Gly Pro Gly Leu Ile Ile Ser Thr Gln Glu Gln
 130 135 140
 Gly Pro Asp Glu Gly Glu Glu Lys Ala Ala Gly Glu Ala Glu Glu Glu
 145 150 155 160
 Glu Glu Asp Asp Asp Asp Glu Glu Glu Glu Glu Asp Leu Ser Ser Pro
 165 170 175
 Pro Gly Leu Pro Glu Pro Leu Glu Ser Val Glu Ala Pro Pro Arg Pro
 180 185 190
 Gln Ala Leu Thr Asp Gly Pro Arg Glu His Ser Lys Ser Ala Ser Leu
 195 200 205
 Leu Phe Gly Met Arg Asn Ser Ala Ala Ser Asp Glu Asp Ser Ser Trp
 210 215 220
 Ala Thr Leu Ser Gln Gly Ser Pro Ser Tyr Gly Ser Pro Glu Asp Thr
 225 230 235 240
 Ala His Leu Asp Arg Phe Cys Ser Trp Arg Arg Leu
 245 250

<210> 166

<211> 665

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 166

Met Ser Val Pro Ser Ser Leu Ser Gln Ser Ala Ile Asn Ala Asn Ser
 1 5 10 15

His Gly Gly Pro Ala Leu Ser Leu Pro Leu Pro Leu His Ala Ala His
 20 25 30

Asn Gln Leu Leu Asn Ala Lys Leu Gln Ala Thr Ala Val Gly Pro Lys
 35 40 45

Asp Leu Arg Ser Ala Met Gly Glu Gly Gly Gly Pro Glu Pro Gly Pro
50 55 60

Ala Asn Ala Lys Trp Leu Lys Glu Gly Gln Asn Gln Leu Arg Arg Ala
65 70 75 80

Ala Thr Ala His Arg Asp Gln Asn Arg Asn Val Thr Leu Thr Leu Ala
85 90 95

Glu Glu Ala Ser Gln Glu Pro Glu Met Ala Pro Leu Gly Pro Lys Gly
100 105 110

Leu Ile His Leu Tyr Ser Glu Leu Glu Leu Ser Ala His Asn Ala Ala
115 120 125

Asn Arg Gly Leu Arg Gly Pro Gly Leu Ile Ile Ser Thr Gln Glu Gln
130 135 140

Gly Pro Asp Glu Gly Glu Glu Lys Ala Ala Gly Glu Ala Glu Glu Glu
145 150 155 160

Glu Glu Asp Asp Asp Asp Glu Glu Glu Glu Glu Asp Leu Ser Ser Pro
165 170 175

Pro Gly Leu Pro Glu Pro Leu Glu Ser Val Glu Ala Pro Pro Arg Pro
180 185 190

Gln Ala Leu Thr Asp Gly Pro Arg Glu His Ser Lys Ser Ala Ser Leu
195 200 205

Leu Phe Gly Met Arg Asn Ser Ala Ala Ser Asp Glu Asp Ser Ser Trp
210 215 220

Ala Thr Leu Ser Gln Gly Ser Pro Ser Tyr Gly Ser Pro Glu Asp Thr
225 230 235 240

Asp Ser Phe Trp Asn Pro Asn Ala Phe Glu Thr Asp Ser Asp Leu Pro
245 250 255

Ala Gly Trp Met Arg Val Gln Asp Thr Ser Gly Thr Tyr Trp His
260 265 270

Ile Pro Thr Gly Thr Thr Gln Trp Glu Pro Pro Gly Arg Ala Ser Pro
275 280 285

Ser Gln Gly Ser Ser Pro Gln Glu Glu Ser Gln Leu Thr Trp Thr Gly
290 295 300

Phe Ala His Gly Glu Gly Phe Glu Asp Gly Glu Phe Trp Lys Asp Glu
305 310 315 320

Pro Ser Asp Glu Ala Pro Met Glu Leu Gly Leu Lys Glu Pro Glu Glu
325 330 335

Gly Thr Leu Thr Phe Pro Ala Gln Ser Leu Ser Pro Glu Pro Leu Pro
340 345 350

Gln Glu Glu Glu Lys Leu Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys

355 360 365
Gly Gly Trp Gly Glu Gly Lys Asp Leu Leu Leu Gln Leu Glu Asp Glu
370 375 380
Thr Leu Lys Leu Val Glu Pro Gln Ser Gln Ala Leu Leu His Ala Gln
385 390 395 400
Pro Ile Ile Ser Ile Arg Val Trp Gly Val Gly Arg Asp Ser Gly Arg
405 410 415
Glu Arg Asp Phe Ala Tyr Val Ala Arg Asp Lys Leu Thr Gln Met Leu
420 425 430
Lys Cys His Val Phe Arg Cys Glu Ala Pro Ala Lys Asn Ile Ala Thr
435 440 445
Ser Leu His Glu Ile Cys Ser Lys Ile Met Ala Glu Arg Arg Asn Ala
450 455 460
Arg Cys Leu Val Asn Gly Leu Ser Leu Asp His Ser Lys Leu Val Asp
465 470 475 480
Val Pro Phe Gln Val Glu Phe Pro Ala Pro Lys Asn Glu Leu Val Gln
485 490 495
Lys Phe Gln Val Tyr Tyr Leu Gly Asn Val Pro Val Ala Lys Pro Val
500 505 510
Gly Val Asp Val Ile Asn Gly Ala Leu Glu Ser Val Leu Ser Ser Ser
515 520 525
Ser Arg Glu Gln Trp Thr Pro Ser His Val Ser Val Ala Pro Ala Thr
530 535 540
Leu Thr Ile Leu His Gln Gln Thr Glu Ala Val Leu Gly Glu Cys Arg
545 550 555 560
Val Arg Phe Leu Ser Phe Leu Ala Val Gly Arg Asp Val His Thr Phe
565 570 575
Ala Phe Ile Met Ala Ala Gly Pro Ala Ser Phe Cys Cys His Met Phe
580 585 590
Trp Cys Glu Pro Asn Ala Ala Ser Leu Ser Glu Ala Val Gln Ala Ala
595 600 605
Cys Met Leu Arg Tyr Gln Lys Cys Leu Asp Ala Arg Ser Gln Ala Ser
610 615 620
Thr Ser Cys Leu Pro Ala Pro Pro Ala Glu Ser Val Ala Arg Arg Val
625 630 635 640
Gly Trp Thr Val Arg Arg Gly Val Gln Ser Leu Trp Gly Ser Leu Lys
645 650 655
Pro Lys Arg Leu Gly Ala His Thr Pro
660 665

<210> 167
 <211> 671
 <212> PRT
 <213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 167

Met Ser Val Pro Ser Ser Leu Ser Gln Ser Ala Ile Asn Ala Asn Ser
 1 5 10 15

His Gly Gly Pro Ala Leu Ser Leu Pro Leu Pro Leu His Ala Ala His
 20 25 30

Asn Gln Leu Leu Asn Ala Lys Leu Gln Ala Thr Ala Val Gly Pro Lys
 35 40 45

Asp Leu Arg Ser Ala Met Gly Glu Gly Gly Gly Pro Glu Pro Gly Pro
 50 55 60

Ala Asn Ala Lys Trp Leu Lys Glu Gly Gln Asn Gln Leu Arg Arg Ala
 65 70 75 80

Ala Thr Ala His Arg Asp Gln Asn Arg Asn Val Thr Leu Thr Leu Ala
 85 90 95

Glu Glu Ala Ser Gln Glu Pro Glu Met Ala Pro Leu Gly Pro Lys Gly
 100 105 110

Leu Ile His Leu Tyr Ser Glu Leu Glu Leu Ser Ala His Asn Ala Ala
 115 120 125

Asn Arg Gly Leu Arg Gly Pro Gly Leu Ile Ile Ser Thr Gln Glu Gln
 130 135 140

Gly Pro Asp Glu Gly Glu Glu Lys Ala Ala Gly Glu Ala Glu Glu Glu
 145 150 155 160

Glu Glu Asp Asp Asp Asp Glu Glu Glu Glu Glu Asp Leu Ser Ser Pro
 165 170 175

Pro Gly Leu Pro Glu Pro Leu Glu Ser Val Glu Ala Pro Pro Arg Pro
 180 185 190

Gln Ala Leu Thr Asp Gly Pro Arg Glu His Ser Lys Ser Ala Ser Leu
 195 200 205

Leu Phe Gly Met Arg Asn Ser Ala Ala Ser Asp Glu Asp Ser Ser Trp
 210 215 220

Ala Thr Leu Ser Gln Gly Ser Pro Ser Tyr Gly Ser Pro Glu Asp Thr
 225 230 235 240

Asp Ser Phe Trp Asn Pro Asn Ala Phe Glu Thr Asp Ser Asp Leu Pro
 245 250 255

Ala Gly Trp Met Arg Val Gln Asp Thr Ser Gly Thr Tyr Trp His

260 265 270
Ile Pro Thr Gly Thr Thr Gln Trp Glu Pro Pro Gly Arg Ala Ser Pro
275 280 285
Ser Gln Gly Ser Ser Pro Gln Glu Glu Ser Gln Leu Thr Trp Thr Gly
290 295 300
Phe Ala His Gly Glu Gly Phe Glu Asp Gly Glu Phe Trp Lys Asp Glu
305 310 315 320
Pro Ser Asp Glu Ala Pro Met Glu Leu Gly Leu Lys Glu Pro Glu Glu
325 330 335
Gly Thr Leu Thr Phe Pro Ala Gln Ser Leu Ser Pro Glu Pro Leu Pro
340 345 350
Gln Glu Glu Glu Lys Leu Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys
355 360 365
Cys Phe Ala Val Arg Ser Leu Gly Trp Val Glu Met Thr Glu Glu Glu
370 375 380
Leu Ala Pro Gly Arg Ser Ser Val Ala Val Asn Asn Cys Ile Arg Gln
385 390 395 400
Leu Ser Tyr His Lys Asn Asn Leu His Asp Pro Met Ser Gly Gly Trp
405 410 415
Gly Glu Gly Lys Asp Leu Leu Leu Gln Leu Glu Asp Glu Thr Leu Lys
420 425 430
Leu Val Glu Pro Gln Ser Gln Ala Leu Leu His Ala Gln Pro Ile Ile
435 440 445
Ser Ile Arg Val Trp Gly Val Gly Arg Asp Ser Gly Arg Glu Ile Met
450 455 460
Ala Glu Arg Arg Asn Ala Arg Cys Leu Val Asn Gly Leu Ser Leu Asp
465 470 475 480
His Ser Lys Leu Val Asp Val Pro Phe Gln Val Glu Phe Pro Ala Pro
485 490 495
Lys Asn Glu Leu Val Gln Lys Phe Gln Val Tyr Tyr Leu Gly Asn Val
500 505 510
Pro Val Ala Lys Pro Val Gly Val Asp Val Ile Asn Gly Ala Leu Glu
515 520 525
Ser Val Leu Ser Ser Ser Ser Arg Glu Gln Trp Thr Pro Ser His Val
530 535 540
Ser Val Ala Pro Ala Thr Leu Thr Ile Leu His Gln Gln Thr Glu Ala
545 550 555 560
Val Leu Gly Glu Cys Arg Val Arg Phe Leu Ser Phe Leu Ala Val Gly
565 570 575

Arg Asp Val His Thr Phe Ala Phe Ile Met Ala Ala Gly Pro Ala Ser
580 585 590

Phe Cys Cys His Met Phe Trp Cys Glu Pro Asn Ala Ala Ser Leu Ser
595 600 605

Glu Ala Val Gln Ala Ala Cys Met Leu Arg Tyr Gln Lys Cys Leu Asp
610 615 620

Ala Arg Ser Gln Ala Ser Thr Ser Cys Leu Pro Ala Pro Pro Ala Glu
625 630 635 640

Ser Val Ala Arg Arg Val Gly Trp Thr Val Arg Arg Gly Val Gln Ser
645 650 655

Leu Trp Gly Ser Leu Lys Pro Lys Arg Leu Gly Ala His Thr Pro
660 665 670

<210> 168

<211> 530

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 168

Met Ser Val Pro Ser Ser Leu Ser Gln Ser Ala Ile Asn Ala Asn Ser
1 5 10 15

His Gly Gly Pro Ala Leu Ser Leu Pro Leu Pro Leu His Ala Ala His
20 25 30

Asn Gln Leu Leu Asn Ala Lys Leu Gln Ala Thr Ala Val Gly Pro Lys
35 40 45

Asp Leu Arg Ser Ala Met Gly Glu Gly Gly Gly Pro Glu Pro Gly Pro
50 55 60

Ala Asn Ala Lys Trp Leu Lys Glu Gly Gln Asn Gln Leu Arg Arg Ala
65 70 75 80

Ala Thr Ala His Arg Asp Gln Asn Arg Asn Val Thr Leu Thr Leu Ala
85 90 95

Glu Glu Ala Ser Gln Glu Pro Glu Met Ala Pro Leu Gly Pro Lys Gly
100 105 110

Leu Ile His Leu Tyr Ser Glu Leu Glu Leu Ser Ala His Asn Ala Ala
115 120 125

Asn Arg Gly Leu Arg Gly Pro Gly Leu Ile Ile Ser Thr Gln Glu Gln
130 135 140

Gly Pro Asp Glu Gly Glu Glu Lys Ala Ala Gly Glu Ala Glu Glu Glu
145 150 155 160

Glu Glu Asp Asp Asp Asp Glu Glu Glu Glu Glu Asp Leu Ser Ser Pro

165 170 175
 Pro Gly Leu Pro Glu Pro Leu Glu Ser Val Glu Ala Pro Pro Arg Pro
 180 185 190
 Gln Ala Leu Thr Asp Gly Pro Arg Glu His Ser Lys Ser Ala Ser Leu
 195 200 205
 Leu Phe Gly Met Arg Asn Ser Ala Ala Ser Asp Glu Asp Ser Ser Trp
 210 215 220
 Ala Thr Leu Ser Gln Gly Ser Pro Ser Tyr Gly Ser Pro Glu Asp Thr
 225 230 235 240
 Asp Ser Phe Trp Asn Pro Asn Ala Phe Glu Thr Asp Ser Asp Leu Pro
 245 250 255
 Ala Gly Trp Met Arg Val Gln Asp Thr Ser Gly Thr Tyr Tyr Trp His
 260 265 270
 Ile Pro Thr Gly Thr Thr Gln Trp Glu Pro Pro Gly Arg Ala Ser Pro
 275 280 285
 Ser Gln Gly Ser Ser Pro Gln Glu Glu Ser Gln Leu Thr Trp Thr Gly
 290 295 300
 Phe Ala His Gly Glu Gly Phe Glu Asp Gly Glu Phe Trp Lys Asp Glu
 305 310 315 320
 Pro Ser Asp Glu Ala Pro Met Glu Leu Gly Leu Lys Glu Pro Glu Glu
 325 330 335
 Gly Thr Leu Thr Phe Pro Ala Gln Ser Leu Ser Pro Glu Pro Leu Pro
 340 345 350
 Gln Glu Glu Glu Lys Leu Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys
 355 360 365
 Cys Phe Ala Val Arg Ser Leu Gly Trp Val Glu Met Thr Glu Glu Glu
 370 375 380
 Leu Ala Pro Gly Arg Ser Ser Val Ala Val Asn Asn Cys Ile Arg Gln
 385 390 395 400
 Leu Ser Tyr His Lys Asn Asn Leu His Asp Pro Met Ser Gly Gly Trp
 405 410 415
 Gly Glu Gly Lys Asp Leu Leu Leu Gln Leu Glu Asp Glu Thr Leu Lys
 420 425 430
 Leu Val Glu Pro Gln Ser Gln Ala Leu Leu His Ala Gln Pro Ile Ile
 435 440 445
 Ser Ile Arg Val Trp Gly Val Gly Arg Asp Ser Gly Arg Glu Arg Asp
 450 455 460
 Phe Ala Tyr Val Ala Arg Asp Lys Leu Thr Gln Met Leu Lys Cys His
 465 470 475 480

Val Phe Arg Cys Glu Ala Pro Ala Lys Asn Ile Ala Thr Ser Leu His
485 490 495

Glu Ile Cys Ser Lys Trp Asn Ser Gln Arg Leu Arg Met Ser Trp Ser
500 505 510

Arg Ser Ser Lys Ser Ile Thr Trp Gly Met Tyr Leu Leu Leu Asn Leu
515 520 525

Leu Gly
530

<210> 169

<211> 639

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 169

Met Ser Val Pro Ser Ser Leu Ser Gln Ser Ala Ile Asn Ala Asn Ser
1 5 10 15

His Gly Gly Pro Ala Leu Ser Leu Pro Leu Pro Leu His Ala Ala His
20 25 30

Asn Gln Leu Leu Asn Ala Lys Leu Gln Ala Thr Ala Val Gly Pro Lys
35 40 45

Asp Leu Arg Ser Ala Met Gly Glu Gly Gly Gly Pro Glu Pro Gly Pro
50 55 60

Ala Asn Ala Lys Trp Leu Lys Glu Gly Gln Asn Gln Leu Arg Arg Ala
65 70 75 80

Ala Thr Ala His Arg Asp Gln Asn Arg Asn Val Thr Leu Thr Leu Ala
85 90 95

Glu Glu Ala Ser Gln Glu Pro Glu Met Ala Pro Leu Gly Pro Lys Gly
100 105 110

Leu Ile His Leu Tyr Ser Glu Leu Glu Leu Ser Ala His Asn Ala Ala
115 120 125

Asn Arg Gly Leu Arg Gly Pro Gly Leu Ile Ile Ser Thr Gln Glu Gln
130 135 140

Gly Pro Asp Glu Gly Glu Lys Ala Ala Gly Glu Ala Glu Glu Glu
145 150 155 160

Glu Glu Asp Asp Asp Asp Glu Glu Glu Glu Glu Asp Leu Ser Ser Pro
165 170 175

Pro Gly Leu Pro Glu Pro Leu Glu Ser Val Glu Ala Pro Pro Arg Pro
180 185 190

Gln Ala Leu Thr Asp Gly Pro Arg Glu His Ser Lys Ser Ala Ser Leu

195	200	205
Leu Phe Gly Met Arg Asn Ser Ala Ala Ser Asp Glu Asp Ser Ser Trp 210 215 220		
Ala Thr Leu Ser Gln Gly Ser Pro Ser Tyr Gly Ser Pro Glu Asp Thr 225 230 235 240		
Asp Ser Phe Trp Asn Pro Asn Ala Phe Glu Thr Asp Ser Asp Leu Pro 245 250 255		
Ala Gly Trp Met Arg Val Gln Asp Thr Ser Gly Thr Tyr Tyr Trp His 260 265 270		
Ile Pro Thr Gly Thr Thr Gln Trp Glu Pro Pro Gly Arg Ala Ser Pro 275 280 285		
Ser Gln Gly Ser Ser Pro Gln Glu Glu Ser Gln Leu Thr Trp Thr Gly 290 295 300		
Phe Ala His Gly Glu Gly Phe Glu Asp Gly Glu Phe Trp Lys Asp Glu 305 310 315 320		
Pro Ser Asp Glu Ala Pro Met Glu Leu Gly Leu Lys Glu Pro Glu Glu 325 330 335		
Gly Thr Leu Thr Phe Pro Ala Gln Ser Leu Ser Pro Glu Pro Leu Pro 340 345 350		
Gln Glu Glu Glu Lys Leu Pro Pro Arg Asn Thr Asn Pro Gly Ile Lys 355 360 365		
Cys Phe Ala Val Arg Ser Leu Gly Trp Val Glu Met Thr Glu Glu Glu 370 375 380		
Leu Ala Pro Gly Arg Ser Ser Val Ala Val Asn Asn Cys Ile Arg Gln 385 390 395 400		
Leu Ser Tyr His Lys Asn Asn Leu His Asp Pro Met Ser Gly Gly Trp 405 410 415		
Gly Glu Gly Lys Asp Leu Leu Leu Gln Leu Glu Asp Glu Thr Leu Lys 420 425 430		
Leu Val Glu Pro Gln Ser Gln Ala Leu Leu His Ala Gln Pro Ile Ile 435 440 445		
Ser Ile Arg Val Trp Gly Val Gly Arg Asp Ser Gly Arg Glu Arg Asp 450 455 460		
Phe Ala Tyr Val Ala Arg Asp Lys Leu Thr Gln Met Leu Lys Cys His 465 470 475 480		
Val Phe Arg Cys Glu Ala Pro Ala Lys Asn Ile Ala Thr Ser Leu His 485 490 495		
Glu Ile Cys Ser Lys Ile Met Ala Glu Arg Arg Asn Ala Arg Cys Leu 500 505 510		

Val Asn Gly Leu Ser Leu Asp His Ser Lys Leu Val Asp Val Pro Phe
515 520 525

Gln Val Glu Phe Pro Ala Pro Lys Asn Glu Leu Val Gln Lys Phe Gln
530 535 540

Val Tyr Tyr Leu Gly Asn Val Pro Val Ala Lys Pro Val Asp Arg Gly
545 550 555 560

Ser Ala Gly Arg Val Ser Gly Ala Phe Pro Leu Leu Pro Gly Arg Gly
565 570 575

Gln Arg Cys Pro His Val Cys Ile His His Gly Cys Arg Pro Ser Leu
580 585 590

Leu Leu Leu Pro His Val Leu Val Arg Ala Gln Cys Cys Gln Pro Leu
595 600 605

Arg Gly Cys Ala Gly Cys Val His Ala Ser Leu Pro Glu Val Ser Gly
610 615 620

Cys Pro Phe Pro Gly Leu His Leu Leu Pro Pro Ser Thr Pro Cys
625 630 635

<210> 170

<211> 50

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 170

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro
20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser
35 40 45

Ser Asp
50

<210> 171

<211> 341

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 171

Met Arg Pro His Leu Ser Pro Pro Leu Gln Gln Leu Leu Leu Pro Val
1 5 10 15

Leu Leu Ala Cys Ala Ala His Ser Thr Gly Ala Leu Pro Arg Leu Cys
20 25 30

Asp Val Leu Gln Val Leu Trp Glu Glu Gln Asp Gln Cys Leu Gln Glu
 35 40 45
 Leu Ser Arg Glu Gln Thr Gly Asp Leu Gly Thr Glu Gln Pro Val Pro
 50 55 60
 Gly Cys Glu Gly Met Trp Asp Asn Ile Ser Cys Trp Pro Ser Ser Val
 65 70 75 80
 Pro Gly Arg Met Val Glu Val Glu Cys Pro Arg Phe Leu Arg Met Leu
 85 90 95
 Thr Ser Arg Asn Gly Ser Leu Phe Arg Asn Cys Thr Gln Asp Gly Trp
 100 105 110
 Ser Glu Thr Phe Pro Arg Pro Asn Leu Ala Cys Gly Val Asn Val Asn
 115 120 125
 Asp Ser Ser Asn Glu Lys Arg His Ser Tyr Leu Leu Lys Leu Lys Val
 130 135 140
 Met Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
 145 150 155 160
 Leu Gly Ile Leu Cys Ala Phe Arg Arg Leu His Cys Thr Arg Asn Tyr
 165 170 175
 Ile His Met His Leu Phe Val Ser Phe Ile Leu Arg Ala Leu Ser Asn
 180 185 190
 Phe Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys
 195 200 205
 Asp Ala His Arg Ala Gly Cys Lys Leu Val Met Val Leu Phe Gln Tyr
 210 215 220
 Cys Ile Met Ala Asn Tyr Ser Trp Leu Leu Val Glu Gly Leu Tyr Leu
 225 230 235 240
 His Thr Leu Leu Ala Ile Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln
 245 250 255
 Gly Phe Val Ala Phe Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu
 260 265 270
 Trp Ala Ile Ala Arg His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile
 275 280 285
 Asn Ala Asn Ala Ser Ile Trp Trp Ile Ile Arg Gly Pro Val Ile Leu
 290 295 300
 Ser Ile Leu Ala Pro Gly Gln Val His Ser Pro Ala Asp Pro Pro Leu
 305 310 315 320
 Trp His Pro Leu His Arg Leu Arg Leu Leu Pro Arg Gly Arg Tyr Gly
 325 330 335

Asp Pro Ala Val Phe
340

<210> 172
<211> 136
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 172

Met Ser Lys Ser Leu Lys Lys Leu Val Glu Glu Ser Arg Glu Lys Asn
1 5 10 15

Gln Pro Glu Val Asp Met Ser Asp Arg Gly Ile Ser Asn Met Leu Asp
20 25 30

Val Asn Gly Leu Phe Thr Leu Ser His Ile Thr Gln Leu Val Leu Ser
35 40 45

His Asn Lys Leu Thr Met Val Pro Pro Asn Ile Ala Glu Leu Lys Asn
50 55 60

Leu Glu Val Leu Asn Phe Phe Asn Asn Gln Ile Glu Glu Leu Pro Thr
65 70 75 80

Gln Ile Ser Ser Leu Gln Lys Leu Lys His Leu Asn Leu Gly Met Asn
85 90 95

Arg Leu Asn Thr Leu Pro Arg Gly Phe Gly Ser Leu Pro Ala Leu Glu
100 105 110

Val Leu Asp Leu Thr Tyr Asn Asn Leu Ser Glu Asn Ser Leu Pro Gly
115 120 125

Asn Phe Phe Tyr Leu Thr Gln Pro
130 135

<210> 173
<211> 488
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 173

Met Asn Cys Arg Glu Leu Pro Leu Thr Leu Trp Val Leu Ile Ser Val
1 5 10 15

Ser Thr Ala Glu Ser Cys Thr Ser Arg Pro His Ile Thr Val Val Glu
20 25 30

Gly Glu Pro Phe Tyr Leu Lys His Cys Ser Cys Ser Leu Ala His Glu
35 40 45

Ile Glu Thr Thr Thr Lys Ser Trp Tyr Lys Ser Ser Gly Ser Gln Glu
50 55 60

His Val Glu Leu Asn Pro Arg Ser Ser Ser Arg Ile Ala Leu His Asp

65 70 75 80
Cys Val Leu Glu Phe Trp Pro Val Glu Leu Asn Asp Thr Gly Ser Tyr
 85 90 95
Phe Phe Gln Met Lys Asn Tyr Thr Gln Lys Trp Lys Leu Asn Val Ile
 100 105 110
Arg Arg Asn Lys His Ser Cys Phe Thr Glu Arg Gln Val Thr Ser Lys
 115 120 125
Ile Val Glu Val Lys Lys Phe Phe Gln Ile Thr Cys Glu Asn Ser Tyr
 130 135 140
Tyr Gln Thr Leu Val Asn Ser Thr Ser Leu Tyr Lys Asn Cys Lys Lys
 145 150 155 160
Leu Leu Leu Glu Asn Asn Lys Asn Pro Thr Ile Lys Lys Asn Ala Glu
 165 170 175
Phe Glu Asp Gln Gly Tyr Tyr Ser Cys Val His Phe Leu His His Asn
 180 185 190
Gly Lys Leu Phe Asn Ile Thr Lys Thr Phe Asn Ile Thr Ile Val Glu
 195 200 205
Asp Arg Ser Asn Ile Val Pro Val Leu Leu Gly Pro Lys Leu Asn His
 210 215 220
Val Ala Val Glu Leu Gly Lys Asn Val Arg Leu Asn Cys Ser Ala Leu
 225 230 235 240
Leu Asn Glu Glu Asp Val Ile Tyr Trp Met Phe Gly Glu Glu Asn Gly
 245 250 255
Ser Asp Pro Asn Ile His Glu Glu Lys Glu Met Arg Ile Met Thr Pro
 260 265 270
Glu Gly Lys Trp His Ala Ser Lys Val Leu Arg Ile Glu Asn Ile Gly
 275 280 285
Glu Ser Asn Leu Asn Val Leu Tyr Asn Cys Thr Val Ala Ser Thr Gly
 290 295 300
Gly Thr Asp Thr Lys Ser Phe Ile Leu Val Arg Lys Ala Asp Met Ala
 305 310 315 320
Asp Ile Pro Gly His Val Phe Thr Arg Gly Met Ile Ile Ala Val Leu
 325 330 335
Ile Leu Val Ala Val Val Cys Leu Val Thr Val Cys Val Ile Tyr Arg
 340 345 350
Val Asp Leu Val Leu Phe Tyr Arg His Leu Thr Arg Arg Asp Glu Thr
 355 360 365
Leu Thr Ala Val Val Asp Glu Ile His Ser Leu Ile Glu Lys Ser Arg
 370 375 380

Arg Leu Ile Ile Val Leu Ser Lys Ser Tyr Met Ser Asn Glu Val Arg
385 390 395 400

Tyr Glu Leu Glu Ser Gly Leu His Glu Ala Leu Val Glu Arg Lys Ile
405 410 415

Lys Ile Ile Leu Ile Glu Phe Thr Pro Val Thr Asp Phe Thr Phe Leu
420 425 430

Pro Gln Ser Leu Lys Leu Leu Lys Ser His Arg Val Leu Lys Trp Lys
435 440 445

Ala Asp Lys Ser Leu Ser Tyr Asn Ser Arg Phe Trp Lys Asn Leu Leu
450 455 460

Tyr Leu Met Pro Ala Lys Thr Val Lys Pro Gly Arg Asp Glu Pro Glu
465 470 475 480

Val Leu Pro Val Leu Ser Glu Ser
485

<210> 174

<211> 270

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 174

Met His Tyr Cys Val Leu Ser Ala Phe Leu Ile Leu His Leu Val Thr
1 5 10 15

Val Ala Leu Ser Leu Ser Thr Cys Ser Thr Leu Asp Met Asp Gln Phe
20 25 30

Met Arg Lys Arg Ile Glu Ala Ile Arg Gly Gln Ile Leu Ser Lys Leu
35 40 45

Lys Leu Thr Ser Pro Pro Glu Asp Tyr Pro Glu Pro Glu Glu Val Pro
50 55 60

Pro Glu Val Ile Ser Ile Tyr Asn Ser Thr Arg Asp Leu Leu Gln Glu
65 70 75 80

Lys Ala Ser Arg Arg Ala Ala Ala Cys Glu Arg Glu Arg Ser Asp Glu
85 90 95

Glu Tyr Tyr Ala Lys Glu Val Tyr Lys Ile Asp Met Pro Pro Phe Phe
100 105 110

Pro Ser Glu Asn Ala Ile Pro Pro Thr Phe Tyr Arg Pro Tyr Phe Arg
115 120 125

Ile Val Arg Phe Asp Val Ser Ala Met Glu Lys Asn Ala Ser Asn Leu
130 135 140

Val Lys Ala Glu Phe Arg Val Phe Arg Leu Gln Asn Pro Lys Ala Arg

145 150 155 160
Val Pro Glu Gln Arg Ile Glu Leu Tyr Gln Ile Leu Lys Ser Lys Asp
165 170 175
Leu Thr Ser Pro Thr Gln Arg Tyr Ile Asp Ser Lys Val Val Lys Thr
180 185 190
Arg Ala Glu Gly Glu Trp Leu Ser Phe Asp Val Thr Asp Ala Val His
195 200 205
Glu Trp Leu His His Lys Asp Arg Asn Leu Gly Phe Lys Ile Ser Leu
210 215 220
His Cys Pro Cys Cys Thr Phe Val Pro Ser Asn Asn Tyr Ile Ile Pro
225 230 235 240
Asn Lys Ser Glu Glu Leu Glu Ala Arg Phe Ala Glu Met Cys Arg Ile
245 250 255
Ile Ala Ala Tyr Val His Phe Thr Leu Ile Ser Arg Gly Ile
260 265 270
<210> 175
<211> 2050
<212> PRT
<213> Artificial sequence
<220>
<223> A novel predicted alternative spliced variant protein product
<400> 175
Met Phe Asn Leu Met Lys Lys Asp Lys Asp Lys Asp Gly Gly Arg Lys
1 5 10 15
Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Arg Met Ser Ala Ala Glu
20 25 30
Leu Arg Ser Leu Glu Glu Met Ser Leu Arg Arg Gly Phe Phe Asn Leu
35 40 45
Asn Arg Ser Ser Lys Arg Glu Ser Lys Thr Arg Leu Glu Ile Ser Asn
50 55 60
Pro Ile Pro Ile Lys Val Ala Ser Gly Ser Asp Leu His Leu Thr Asp
65 70 75 80
Ile Asp Ser Asp Ser Asn Arg Gly Ser Val Ile Leu Asp Ser Gly His
85 90 95
Leu Ser Thr Ala Ser Ser Ser Asp Asp Leu Lys Gly Glu Glu Gly Ser
100 105 110
Phe Arg Gly Ser Val Leu Gln Arg Ala Ala Lys Phe Gly Ser Leu Ala
115 120 125
Lys Gln Asn Ser Gln Met Ile Val Lys Arg Phe Ser Phe Ser Gln Arg
130 135 140

Ser Arg Asp Glu Ser Ala Ser Glu Thr Ser Thr Pro Ser Glu His Ser
 145 150 155 160
 Ala Ala Pro Ser Pro Gln Val Glu Val Arg Thr Leu Glu Gly Gln Leu
 165 170 175
 Val Gln His Pro Gly Pro Gly Ile Pro Arg Pro Gly His Arg Ser Arg
 180 185 190
 Ala Pro Glu Leu Val Thr Lys Lys Phe Pro Val Asp Leu Arg Leu Pro
 195 200 205
 Pro Val Val Pro Leu Pro Pro Pro Thr Leu Arg Glu Leu Glu Leu Gln
 210 215 220
 Arg Arg Pro Thr Gly Asp Phe Gly Phe Ser Leu Arg Arg Thr Thr Met
 225 230 235 240
 Leu Asp Arg Gly Pro Glu Gly Gln Ala Cys Arg Arg Val Val His Phe
 245 250 255
 Ala Glu Pro Gly Ala Gly Thr Lys Asp Leu Ala Leu Gly Leu Val Pro
 260 265 270
 Gly Asp Arg Leu Val Glu Ile Asn Gly His Asn Val Glu Ser Lys Ser
 275 280 285
 Arg Asp Glu Ile Val Glu Met Ile Arg Gln Ser Gly Asp Ser Val Arg
 290 295 300
 Leu Lys Val Gln Pro Ile Pro Glu Leu Ser Glu Leu Ser Arg Ser Trp
 305 310 315 320
 Leu Arg Ser Gly Glu Gly Pro Arg Arg Glu Pro Ser Asp Ala Lys Thr
 325 330 335
 Glu Glu Gln Ile Ala Ala Glu Glu Ala Trp Asn Glu Thr Glu Lys Val
 340 345 350
 Trp Leu Val His Arg Asp Gly Phe Ser Leu Ala Ser Gln Leu Lys Ser
 355 360 365
 Glu Glu Leu Asn Leu Pro Glu Gly Lys Val Arg Val Lys Leu Asp His
 370 375 380
 Asp Gly Ala Ile Leu Asp Val Asp Glu Asp Asp Val Glu Lys Ala Asn
 385 390 395 400
 Ala Pro Ser Cys Asp Arg Leu Glu Asp Leu Ala Ser Leu Val Tyr Leu
 405 410 415
 Asn Glu Ser Ser Val Leu His Thr Leu Arg Gln Arg Tyr Gly Ala Ser
 420 425 430
 Leu Leu His Thr Tyr Ala Gly Pro Ser Leu Leu Val Leu Gly Pro Arg
 435 440 445
 Gly Ala Pro Ala Val Tyr Ser Glu Lys Val Met His Met Phe Lys Gly

450 455 460
Cys Arg Arg Glu Asp Met Ala Pro His Ile Tyr Ala Val Ala Gln Thr
465 470 475 480
Ala Tyr Arg Ala Met Leu Met Ser Arg Gln Asp Gln Ser Ile Ile Leu
485 490 495
Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Ser Cys Gln His Leu Val
500 505 510
Gln Tyr Leu Ala Thr Ile Ala Gly Ile Ser Gly Asn Lys Val Phe Ser
515 520 525
Val Glu Lys Trp Gln Ala Leu Tyr Thr Leu Leu Glu Ala Phe Gly Asn
530 535 540
Ser Pro Thr Ile Ile Asn Gly Asn Ala Thr Arg Phe Ser Gln Ile Leu
545 550 555 560
Ser Leu Asp Phe Asp Gln Ala Gly Gln Val Ala Ser Ala Ser Ile Gln
565 570 575
Thr Met Leu Leu Glu Lys Leu Arg Val Ala Arg Arg Pro Ala Ser Glu
580 585 590
Ala Thr Phe Asn Val Phe Tyr Tyr Leu Leu Ala Cys Gly Asp Gly Thr
595 600 605
Leu Arg Thr Glu Leu His Leu Asn His Leu Ala Glu Asn Asn Val Phe
610 615 620
Gly Ile Val Pro Leu Ala Lys Pro Glu Glu Lys Gln Lys Ala Ala Gln
625 630 635 640
Gln Phe Ser Lys Leu Gln Ala Ala Met Lys Val Leu Gly Ile Ser Pro
645 650 655
Asp Glu Gln Lys Ala Cys Trp Phe Ile Leu Ala Ala Ile Tyr His Leu
660 665 670
Gly Ala Ala Gly Ala Thr Lys Ala Gly Arg Lys Gln Phe Ala Arg His
675 680 685
Glu Trp Ala Gln Lys Ala Ala Tyr Leu Leu Gly Cys Ser Leu Glu Glu
690 695 700
Leu Ser Ser Ala Ile Phe Lys His Gln His Lys Gly Gly Thr Leu Gln
705 710 715 720
Arg Ser Thr Ser Phe Arg Gln Gly Pro Glu Glu Ser Gly Leu Gly Asp
725 730 735
Gly Thr Gly Pro Lys Leu Ser Ala Leu Glu Cys Leu Glu Gly Met Ala
740 745 750
Ala Gly Leu Tyr Ser Glu Leu Phe Thr Leu Leu Val Ser Leu Val Asn
755 760 765

Arg Ala Leu Lys Ser Ser Gln His Ser Leu Cys Ser Met Met Ile Val
 770 775 780
 Asp Thr Pro Gly Phe Gln Asn Pro Glu Gln Gly Gly Ser Ala Arg Gly
 785 790 795 800
 Ala Ser Phe Glu Glu Leu Cys His Asn Tyr Thr Gln Asp Arg Leu Gln
 805 810 815
 Arg Leu Phe His Glu Arg Thr Phe Val Gln Glu Leu Glu Arg Tyr Lys
 820 825 830
 Glu Glu Asn Ile Glu Leu Ala Phe Asp Asp Leu Glu Pro Pro Thr Asp
 835 840 845
 Asp Ser Val Ala Ala Val Asp Gln Ala Ser His Gln Ser Leu Val Arg
 850 855 860
 Ser Leu Ala Arg Thr Asp Glu Ala Arg Gly Leu Leu Trp Leu Leu Glu
 865 870 875 880
 Glu Glu Ala Leu Val Pro Gly Ala Ser Glu Asp Thr Leu Leu Glu Arg
 885 890 895
 Leu Phe Ser Tyr Tyr Gly Pro Gln Glu Gly Asp Lys Lys Gly Gln Ser
 900 905 910
 Pro Leu Leu His Ser Ser Lys Pro His His Phe Leu Leu Gly His Ser
 915 920 925
 His Gly Thr Asn Trp Val Glu Tyr Asn Val Thr Gly Trp Leu Asn Tyr
 930 935 940
 Thr Lys Gln Asn Pro Ala Thr Gln Asn Ala Pro Arg Leu Leu Gln Asp
 945 950 955 960
 Ser Gln Lys Lys Ile Ile Ser Asn Leu Phe Leu Gly Arg Ala Gly Ser
 965 970 975
 Ala Thr Val Leu Ser Gly Ser Ile Ala Gly Leu Glu Gly Gly Ser Gln
 980 985 990
 Leu Ala Leu Arg Arg Ala Thr Ser Met Arg Lys Thr Phe Thr Thr Gly
 995 1000 1005
 Met Ala Ala Val Lys Lys Lys Ser Leu Cys Ile Gln Met Lys Leu
 1010 1015 1020
 Gln Val Asp Ala Leu Ile Asp Thr Ile Lys Lys Ser Lys Leu His
 1025 1030 1035
 Phe Val His Cys Phe Leu Pro Val Ala Glu Gly Trp Ala Gly Glu
 1040 1045 1050
 Pro Arg Ser Ala Ser Ser Arg Arg Val Ser Ser Ser Ser Glu Leu
 1055 1060 1065

Asp Leu Pro Ser Gly Asp His Cys Glu Ala Gly Leu Leu Gln Leu
 1070 1075 1080
 Asp Val Pro Leu Leu Arg Thr Gln Leu Arg Gly Ser Arg Leu Leu
 1085 1090 1095
 Asp Ala Met Arg Met Tyr Arg Gln Gly Tyr Pro Asp His Met Val
 1100 1105 1110
 Phe Ser Glu Phe Arg Arg Arg Phe Asp Val Leu Ala Pro His Leu
 1115 1120 1125
 Thr Lys Lys His Gly Arg Asn Tyr Ile Val Val Asp Glu Arg Arg
 1130 1135 1140
 Ala Val Glu Glu Leu Leu Glu Cys Leu Asp Leu Glu Lys Ser Ser
 1145 1150 1155
 Cys Cys Met Gly Leu Ser Arg Val Phe Phe Arg Ala Gly Thr Leu
 1160 1165 1170
 Ala Arg Leu Glu Glu Gln Arg Asp Glu Gln Thr Ser Arg Asn Leu
 1175 1180 1185
 Thr Leu Phe Gln Ala Ala Cys Arg Gly Tyr Leu Ala Arg Gln His
 1190 1195 1200
 Phe Lys Lys Arg Lys Ile Gln Asp Leu Ala Ile Arg Cys Val Gln
 1205 1210 1215
 Lys Asn Ile Lys Lys Asn Lys Gly Val Lys Asp Trp Pro Trp Trp
 1220 1225 1230
 Lys Leu Phe Thr Thr Val Arg Pro Leu Ile Glu Val Gln Leu Ser
 1235 1240 1245
 Glu Glu Gln Ile Arg Asn Lys Asp Glu Glu Ile Gln Gln Leu Arg
 1250 1255 1260
 Ser Lys Leu Glu Lys Ala Glu Lys Glu Arg Asn Glu Leu Arg Leu
 1265 1270 1275
 Asn Ser Asp Arg Leu Glu Ser Arg Ile Ser Glu Leu Thr Ser Glu
 1280 1285 1290
 Leu Thr Asp Glu Arg Asn Thr Gly Glu Ser Ala Ser Gln Leu Leu
 1295 1300 1305
 Asp Ala Glu Thr Ala Glu Arg Leu Arg Ala Glu Lys Glu Met Lys
 1310 1315 1320
 Glu Leu Gln Thr Gln Tyr Asp Ala Leu Lys Lys Gln Met Glu Val
 1325 1330 1335
 Met Glu Met Glu Val Met Glu Ala Arg Leu Ile Arg Ala Ala Glu
 1340 1345 1350

Ile Asn Gly Glu Val Asp Asp Asp Asp Ala Gly Gly Glu Trp Arg
1355 1360 1365

Leu Lys Tyr Glu Arg Ala Val Arg Glu Val Asp Phe Thr Lys Lys
1370 1375 1380

Arg Leu Gln Gln Glu Phe Glu Asp Lys Leu Glu Val Glu Gln Gln
1385 1390 1395

Asn Lys Arg Gln Leu Glu Arg Arg Leu Gly Asp Leu Gln Ala Asp
1400 1405 1410

Ser Glu Glu Ser Gln Arg Ala Leu Gln Gln Leu Lys Lys Lys Cys
1415 1420 1425

Gln Arg Leu Thr Ala Glu Leu Gln Asp Thr Lys Leu His Leu Glu
1430 1435 1440

Gly Gln Gln Val Arg Asn His Glu Leu Glu Lys Lys Gln Arg Arg
1445 1450 1455

Phe Asp Ser Glu Leu Ser Gln Ala His Glu Glu Ala Gln Arg Glu
1460 1465 1470

Lys Leu Gln Arg Glu Lys Leu Gln Arg Glu Lys Asp Met Leu Leu
1475 1480 1485

Ala Glu Ala Phe Ser Leu Lys Gln Gln Leu Glu Glu Lys Asp Met
1490 1495 1500

Asp Ile Ala Gly Phe Thr Gln Lys Val Val Ser Leu Glu Ala Glu
1505 1510 1515

Leu Gln Asp Ile Ser Ser Gln Glu Ser Lys Asp Glu Ala Ser Leu
1520 1525 1530

Ala Lys Val Lys Lys Gln Leu Arg Asp Leu Glu Ala Lys Val Lys
1535 1540 1545

Asp Gln Glu Glu Glu Leu Asp Glu Gln Ala Gly Thr Ile Gln Met
1550 1555 1560

Leu Glu Gln Ala Lys Leu Arg Leu Glu Met Glu Met Glu Arg Met
1565 1570 1575

Arg Gln Thr His Ser Lys Glu Met Glu Ser Arg Asp Glu Glu Val
1580 1585 1590

Glu Glu Ala Arg Gln Ser Cys Gln Lys Lys Leu Lys Gln Met Glu
1595 1600 1605

Val Gln Leu Glu Glu Glu Tyr Glu Asp Lys Gln Lys Val Leu Arg
1610 1615 1620

Glu Lys Arg Glu Leu Glu Gly Lys Leu Ala Thr Leu Ser Asp Gln
1625 1630 1635

Val Asn Arg Arg Asp Phe Glu Ser Glu Lys Arg Leu Arg Lys Asp

1640	1645	1650
Leu Lys Arg Thr Lys Ala Leu Leu Ala Asp Ala Gln Leu Met Leu		
1655	1660	1665
Asp His Leu Lys Asn Ser Ala Pro Ser Lys Arg Glu Ile Ala Gln		
1670	1675	1680
Leu Lys Asn Gln Leu Glu Glu Ser Glu Phe Thr Cys Ala Ala Ala		
1685	1690	1695
Val Lys Ala Arg Lys Ala Met Glu Val Glu Ile Glu Asp Leu His		
1700	1705	1710
Leu Gln Ile Asp Asp Ile Ala Lys Ala Lys Thr Ala Leu Glu Glu		
1715	1720	1725
Gln Leu Ser Arg Leu Gln Arg Glu Lys Asn Glu Ile Gln Asn Arg		
1730	1735	1740
Leu Glu Glu Asp Gln Glu Asp Met Asn Glu Leu Met Lys Lys His		
1745	1750	1755
Lys Ala Ala Val Ala Gln Ala Ser Arg Asp Leu Ala Gln Ile Asn		
1760	1765	1770
Asp Leu Gln Ala Gln Leu Glu Glu Ala Asn Lys Glu Lys Gln Glu		
1775	1780	1785
Leu Gln Glu Lys Leu Gln Ala Leu Gln Ser Gln Val Glu Phe Leu		
1790	1795	1800
Glu Gln Ser Met Val Asp Lys Ser Leu Val Ser Arg Gln Glu Ala		
1805	1810	1815
Lys Ile Arg Glu Leu Glu Thr Arg Leu Glu Phe Glu Arg Thr Gln		
1820	1825	1830
Val Lys Arg Leu Glu Ser Leu Ala Ser Arg Leu Lys Glu Asn Met		
1835	1840	1845
Glu Lys Leu Thr Glu Glu Arg Asp Gln Arg Ile Ala Ala Glu Asn		
1850	1855	1860
Arg Glu Lys Glu Gln Asn Lys Arg Leu Gln Arg Gln Leu Arg Asp		
1865	1870	1875
Thr Lys Glu Glu Met Gly Glu Leu Ala Arg Lys Glu Ala Glu Ala		
1880	1885	1890
Ser Arg Lys Lys His Glu Leu Glu Met Asp Leu Glu Ser Leu Glu		
1895	1900	1905
Ala Ala Asn Gln Ser Leu Gln Ala Asp Leu Lys Leu Ala Phe Lys		
1910	1915	1920
Arg Ile Gly Asp Leu Gln Ala Ala Ile Glu Asp Glu Met Glu Ser		
1925	1930	1935

Asp Glu Asn Glu Asp Leu Ile Asn Ser Leu Gln Asp Met Val Thr
1940 1945 1950

Lys Tyr Gln Lys Arg Lys Asn Lys Leu Glu Gly Asp Ser Asp Val
1955 1960 1965

Asp Ser Glu Leu Glu Asp Arg Val Asp Gly Val Lys Ser Trp Leu
1970 1975 1980

Ser Lys Asn Lys Gly Pro Ser Lys Ala Ala Ser Asp Asp Gly Ser
1985 1990 1995

Leu Lys Ser Ser Ser Pro Thr Ser Tyr Trp Lys Ser Leu Ala Pro
2000 2005 2010

Asp Arg Ser Asp Asp Glu His Asp Pro Leu Asp Asn Thr Ser Arg
2015 2020 2025

Pro Arg Tyr Ser His Ser Tyr Leu Ser Asp Ser Asp Thr Glu Ala
2030 2035 2040

Lys Leu Thr Glu Thr Asn Ala
2045 2050

<210> 176

<211> 2014

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 176

Met Phe Asn Leu Met Lys Lys Asp Lys Asp Lys Asp Gly Gly Arg Lys
1 5 10 15

Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Arg Met Ser Ala Ala Glu
20 25 30

Leu Arg Ser Leu Glu Glu Met Ser Leu Arg Arg Gly Phe Phe Asn Leu
35 40 45

Asn Arg Ser Ser Lys Arg Glu Ser Lys Thr Arg Leu Glu Ile Ser Asn
50 55 60

Pro Ile Pro Ile Lys Val Ala Ser Gly Ser Asp Leu His Leu Thr Asp
65 70 75 80

Ile Asp Ser Asp Ser Asn Arg Gly Ser Val Ile Leu Asp Ser Gly His
85 90 95

Leu Ser Thr Ala Ser Ser Ser Asp Asp Leu Lys Gly Glu Glu Gly Ser
100 105 110

Phe Arg Gly Ser Val Leu Gln Arg Ala Ala Lys Phe Gly Ser Leu Ala
115 120 125

Lys Gln Asn Ser Gln Met Ile Val Lys Arg Phe Ser Phe Ser Gln Arg

130 135 140
 Ser Arg Asp Glu Ser Ala Ser Glu Thr Ser Thr Pro Ser Glu His Ser
 145 150 155 160
 Ala Ala Pro Ser Pro Gln Val Glu Val Arg Thr Leu Glu Gly Gln Leu
 165 170 175
 Val Gln His Pro Gly Pro Gly Ile Pro Arg Pro Gly His Arg Ser Arg
 180 185 190
 Ala Pro Glu Leu Val Thr Lys Lys Phe Pro Val Asp Leu Arg Leu Pro
 195 200 205
 Pro Val Val Pro Leu Pro Pro Pro Thr Leu Arg Glu Leu Glu Leu Gln
 210 215 220
 Arg Arg Pro Thr Gly Asp Phe Gly Phe Ser Leu Arg Arg Thr Thr Met
 225 230 235 240
 Leu Asp Arg Gly Pro Glu Gly Gln Ala Cys Arg Arg Val Val His Phe
 245 250 255
 Ala Glu Pro Gly Ala Gly Thr Lys Asp Leu Ala Leu Gly Leu Val Pro
 260 265 270
 Gly Asp Arg Leu Val Glu Ile Asn Gly His Asn Val Glu Ser Lys Ser
 275 280 285
 Arg Asp Glu Ile Val Glu Met Ile Arg Gln Ser Gly Asp Ser Val Arg
 290 295 300
 Leu Lys Val Gln Pro Ile Pro Glu Leu Ser Glu Leu Ser Arg Ser Trp
 305 310 315 320
 Leu Arg Ser Gly Gly Gly Pro Arg Arg Glu Pro Ser Asp Ala Lys Thr
 325 330 335
 Glu Glu Gln Ile Ala Ala Glu Glu Ala Trp Asn Glu Thr Glu Lys Val
 340 345 350
 Trp Leu Val His Arg Asp Gly Phe Ser Leu Ala Ser Gln Leu Lys Ser
 355 360 365
 Glu Glu Leu Asn Leu Pro Glu Gly Lys Val Arg Val Lys Leu Asp His
 370 375 380
 Asp Gly Ala Ile Leu Asp Val Asp Glu Asp Asp Val Glu Lys Ala Asn
 385 390 395 400
 Ala Pro Ser Cys Asp Arg Leu Glu Asp Leu Ala Ser Leu Val Tyr Leu
 405 410 415
 Asn Glu Ser Ser Val Leu His Thr Leu Arg Gln Arg Tyr Gly Ala Ser
 420 425 430
 Leu Leu His Thr Tyr Ala Gly Pro Ser Leu Leu Val Leu Gly Pro Arg
 435 440 445

Gly Ala Pro Ala Val Tyr Ser Glu Lys Val Met His Met Phe Lys Gly
 450 455 460
 Cys Arg Arg Glu Asp Met Ala Pro His Ile Tyr Ala Val Ala Gln Thr
 465 470 475 480
 Ala Tyr Arg Ala Met Leu Met Ser Arg Gln Asp Gln Ser Ile Ile Leu
 485 490 495
 Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Ser Cys Gln His Leu Val
 500 505 510
 Gln Tyr Leu Ala Thr Ile Ala Gly Ile Ser Gly Asn Lys Val Phe Ser
 515 520 525
 Val Glu Lys Trp Gln Ala Leu Tyr Thr Leu Leu Glu Ala Phe Gly Asn
 530 535 540
 Ser Pro Thr Ile Ile Asn Gly Asn Ala Thr Arg Phe Ser Gln Ile Leu
 545 550 555 560
 Ser Leu Asp Phe Asp Gln Ala Gly Gln Val Ala Ser Ala Ser Ile Gln
 565 570 575
 Thr Met Leu Leu Glu Lys Leu Arg Val Ala Arg Arg Pro Ala Ser Glu
 580 585 590
 Ala Thr Phe Asn Val Phe Tyr Tyr Leu Leu Ala Cys Gly Asp Gly Thr
 595 600 605
 Leu Arg Thr Glu Leu His Leu Asn His Leu Ala Glu Asn Asn Val Phe
 610 615 620
 Gly Ile Val Pro Leu Ala Lys Pro Glu Glu Lys Gln Lys Ala Ala Gln
 625 630 635 640
 Gln Phe Ser Lys Leu Gln Ala Ala Met Lys Val Leu Gly Ile Ser Pro
 645 650 655
 Asp Glu Gln Lys Ala Cys Trp Phe Ile Leu Ala Ala Ile Tyr His Leu
 660 665 670
 Gly Ala Ala Gly Ala Thr Lys Glu Ala Ala Glu Ala Gly Arg Lys Gln
 675 680 685
 Phe Ala Arg His Glu Trp Ala Gln Lys Ala Ala Tyr Leu Leu Gly Cys
 690 695 700
 Ser Leu Glu Glu Leu Ser Ser Ala Ile Phe Lys His Gln His Lys Gly
 705 710 715 720
 Gly Thr Leu Gln Arg Ser Thr Ser Phe Arg Gln Gly Pro Glu Glu Ser
 725 730 735
 Gly Leu Gly Asp Gly Thr Gly Pro Lys Leu Ser Ala Leu Glu Cys Leu
 740 745 750

Glu Gly Met Ala Ala Gly Leu Tyr Ser Glu Leu Phe Thr Leu Leu Val
755 760 765

Ser Leu Val Asn Arg Ala Leu Lys Ser Ser Gln His Ser Leu Cys Ser
770 775 780

Met Met Ile Val Asp Thr Pro Gly Phe Gln Asn Pro Glu Gln Gly Gly
785 790 795 800

Ser Ala Arg Gly Ala Ser Phe Glu Glu Leu Cys His Asn Tyr Thr Gln
805 810 815

Asp Arg Leu Gln Arg Leu Phe His Glu Arg Thr Phe Val Gln Glu Leu
820 825 830

Glu Arg Tyr Lys Glu Glu Asn Ile Glu Leu Ala Phe Asp Asp Leu Glu
835 840 845

Pro Pro Thr Asp Asp Ser Val Ala Ala Val Asp Gln Ala Ser His Gln
850 855 860

Ser Leu Val Arg Ser Leu Ala Arg Thr Asp Glu Ala Arg Gly Leu Leu
865 870 875 880

Trp Leu Leu Glu Glu Glu Ala Leu Val Pro Gly Ala Ser Glu Asp Thr
885 890 895

Leu Leu Glu Arg Leu Phe Ser Tyr Tyr Gly Pro Gln Glu Gly Asp Lys
900 905 910

Lys Gly Gln Ser Pro Leu Leu His Ser Ser Lys Pro His His Phe Leu
915 920 925

Leu Gly His Ser His Gly Thr Asn Trp Val Glu Tyr Asn Val Thr Gly
930 935 940

Trp Leu Asn Tyr Thr Lys Gln Asn Pro Ala Thr Gln Asn Ala Pro Arg
945 950 955 960

Leu Leu Gln Asp Ser Gln Lys Lys Ile Ile Ser Asn Leu Phe Leu Gly
965 970 975

Arg Ala Gly Ser Ala Thr Val Leu Ser Gly Ser Ile Ala Gly Leu Glu
980 985 990

Gly Gly Ser Gln Leu Ala Leu Arg Arg Ala Thr Ser Met Arg Lys Thr
995 1000 1005

Phe Thr Thr Gly Met Ala Ala Val Lys Lys Lys Ser Leu Cys Ile
1010 1015 1020

Gln Met Lys Leu Gln Val Asp Ala Leu Ile Asp Thr Ile Lys Lys
1025 1030 1035

Ser Lys Leu His Phe Val His Cys Phe Leu Pro Val Ala Glu Gly
1040 1045 1050

Trp Ala Gly Glu Pro Arg Ser Ala Ser Ser Arg Arg Val Ser Ser
 1055 1060 1065
 Ser Ser Glu Leu Asp Leu Pro Ser Gly Asp His Cys Glu Ala Gly
 1070 1075 1080
 Leu Leu Gln Leu Asp Val Pro Leu Leu Arg Thr Gln Leu Arg Gly
 1085 1090 1095
 Ser Arg Leu Leu Asp Ala Met Arg Met Tyr Arg Gln Gly Tyr Pro
 1100 1105 1110
 Asp His Met Val Phe Ser Glu Phe Arg Arg Arg Phe Asp Val Leu
 1115 1120 1125
 Ala Pro His Leu Thr Lys Lys His Gly Arg Asn Tyr Ile Val Val
 1130 1135 1140
 Asp Glu Arg Arg Ala Val Glu Glu Leu Leu Glu Cys Leu Asp Leu
 1145 1150 1155
 Glu Lys Ser Ser Cys Cys Met Gly Leu Ser Arg Val Phe Phe Arg
 1160 1165 1170
 Ala Gly Thr Leu Ala Arg Leu Glu Glu Gln Arg Asp Glu Gln Thr
 1175 1180 1185
 Ser Arg Asn Leu Thr Leu Phe Gln Ala Ala Cys Arg Gly Tyr Leu
 1190 1195 1200
 Ala Arg Gln His Phe Lys Lys Arg Lys Ile Gln Asp Leu Ala Ile
 1205 1210 1215
 Arg Cys Val Gln Lys Asn Ile Lys Lys Asn Lys Gly Val Lys Asp
 1220 1225 1230
 Trp Pro Trp Trp Lys Leu Phe Thr Thr Val Arg Pro Leu Ile Glu
 1235 1240 1245
 Val Gln Leu Ser Glu Glu Gln Ile Arg Asn Lys Asp Glu Glu Ile
 1250 1255 1260
 Gln Gln Leu Arg Ser Lys Leu Glu Lys Ala Glu Lys Glu Arg Asn
 1265 1270 1275
 Glu Leu Arg Leu Asn Ser Asp Arg Leu Glu Ser Arg Thr Gln Tyr
 1280 1285 1290
 Asp Ala Leu Lys Lys Gln Met Glu Val Met Glu Met Glu Val Met
 1295 1300 1305
 Glu Ala Arg Leu Ile Arg Ala Ala Glu Ile Asn Gly Glu Val Asp
 1310 1315 1320
 Asp Asp Asp Ala Gly Gly Glu Trp Arg Leu Lys Tyr Glu Arg Ala
 1325 1330 1335
 Val Arg Glu Val Asp Phe Thr Lys Lys Arg Leu Gln Gln Glu Phe

1340	1345	1350
Glu Asp Lys Leu Glu Val	Glu Gln Gln Asn Lys	Arg Gln Leu Glu
1355	1360	1365
Arg Arg Leu Gly Asp Leu	Gln Ala Asp Ser Glu	Glu Ser Gln Arg
1370	1375	1380
Ala Leu Gln Gln Leu Lys	Lys Lys Cys Gln Arg	Leu Thr Ala Glu
1385	1390	1395
Leu Gln Asp Thr Lys Leu	His Leu Glu Gly Gln Gln	Val Arg Asn
1400	1405	1410
His Glu Leu Glu Lys Lys	Gln Arg Arg Phe Asp	Ser Glu Leu Ser
1415	1420	1425
Gln Ala His Glu Glu Ala	Gln Arg Glu Lys Leu	Gln Arg Glu Lys
1430	1435	1440
Leu Gln Arg Glu Lys Asp	Met Leu Leu Ala Glu	Ala Phe Ser Leu
1445	1450	1455
Lys Gln Gln Leu Glu Glu	Lys Asp Met Asp Ile	Ala Gly Phe Thr
1460	1465	1470
Gln Lys Val Val Ser Leu	Glu Ala Glu Leu Gln	Asp Ile Ser Ser
1475	1480	1485
Gln Glu Ser Lys Asp Glu	Ala Ser Leu Ala Lys	Val Lys Lys Gln
1490	1495	1500
Leu Arg Asp Leu Glu Ala	Lys Val Lys Asp Gln	Glu Glu Glu Leu
1505	1510	1515
Asp Glu Gln Ala Gly Thr	Ile Gln Met Leu Glu	Gln Ala Lys Leu
1520	1525	1530
Arg Leu Glu Met Glu Met	Glu Arg Met Arg Gln	Thr His Ser Lys
1535	1540	1545
Glu Met Glu Ser Arg Asp	Glu Glu Val Glu Glu	Ala Arg Gln Ser
1550	1555	1560
Cys Gln Lys Lys Leu Lys	Gln Met Glu Val Gln	Leu Glu Glu Glu
1565	1570	1575
Tyr Glu Asp Lys Gln Lys	Val Leu Arg Glu Lys	Arg Glu Leu Glu
1580	1585	1590
Gly Lys Leu Ala Thr Leu	Ser Asp Gln Val Asn	Arg Arg Asp Phe
1595	1600	1605
Glu Ser Glu Lys Arg Leu	Arg Lys Asp Leu Lys	Arg Thr Lys Ala
1610	1615	1620
Leu Leu Ala Asp Ala Gln	Leu Met Leu Asp His	Leu Lys Asn Ser
1625	1630	1635

Ala Pro Ser Lys Arg Glu Ile Ala Gln Leu Lys Asn Gln Leu Glu
 1640 1645 1650
 Glu Ser Glu Phe Thr Cys Ala Ala Ala Val Lys Ala Arg Lys Ala
 1655 1660 1665
 Met Glu Val Glu Ile Glu Asp Leu His Leu Gln Ile Asp Asp Ile
 1670 1675 1680
 Ala Lys Ala Lys Thr Ala Leu Glu Glu Gln Leu Ser Arg Leu Gln
 1685 1690 1695
 Arg Glu Lys Asn Glu Ile Gln Asn Arg Leu Glu Glu Asp Gln Glu
 1700 1705 1710
 Asp Met Asn Glu Leu Met Lys Lys His Lys Ala Ala Val Ala Gln
 1715 1720 1725
 Ala Ser Arg Asp Leu Ala Gln Ile Asn Asp Leu Gln Ala Gln Leu
 1730 1735 1740
 Glu Glu Ala Asn Lys Glu Lys Gln Glu Leu Gln Glu Lys Leu Gln
 1745 1750 1755
 Ala Leu Gln Ser Gln Val Glu Phe Leu Glu Gln Ser Met Val Asp
 1760 1765 1770
 Lys Ser Leu Val Ser Arg Gln Glu Ala Lys Ile Arg Glu Leu Glu
 1775 1780 1785
 Thr Arg Leu Glu Phe Glu Arg Thr Gln Val Lys Arg Leu Glu Ser
 1790 1795 1800
 Leu Ala Ser Arg Leu Lys Glu Asn Met Glu Lys Leu Thr Glu Glu
 1805 1810 1815
 Arg Asp Gln Arg Ile Ala Ala Glu Asn Arg Glu Lys Glu Gln Asn
 1820 1825 1830
 Lys Arg Leu Gln Arg Gln Leu Arg Asp Thr Lys Glu Glu Met Gly
 1835 1840 1845
 Glu Leu Ala Arg Lys Glu Ala Glu Ala Ser Arg Lys Lys His Glu
 1850 1855 1860
 Leu Glu Met Asp Leu Glu Ser Leu Glu Ala Ala Asn Gln Ser Leu
 1865 1870 1875
 Gln Ala Asp Leu Lys Leu Ala Phe Lys Arg Ile Gly Asp Leu Gln
 1880 1885 1890
 Ala Ala Ile Glu Asp Glu Met Glu Ser Asp Glu Asn Glu Asp Leu
 1895 1900 1905
 Ile Asn Ser Leu Gln Asp Met Val Thr Lys Tyr Gln Lys Arg Lys
 1910 1915 1920

Asn Lys Leu Glu Gly Asp Ser Asp Val Asp Ser Glu Leu Glu Asp
1925 1930 1935

Arg Val Asp Gly Val Lys Ser Trp Leu Ser Lys Asn Lys Gly Pro
1940 1945 1950

Ser Lys Ala Ala Ser Asp Asp Gly Ser Leu Lys Ser Ser Ser Pro
1955 1960 1965

Thr Ser Tyr Trp Lys Ser Leu Ala Pro Asp Arg Ser Asp Asp Glu
1970 1975 1980

His Asp Pro Leu Asp Asn Thr Ser Arg Pro Arg Tyr Ser His Ser
1985 1990 1995

Tyr Leu Ser Asp Ser Asp Thr Glu Ala Lys Leu Thr Glu Thr Asn
2000 2005 2010

Ala

<210> 177

<211> 2016

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 177

Met Phe Asn Leu Met Lys Lys Asp Lys Asp Lys Asp Gly Gly Arg Lys
1 5 10 15

Glu Lys Lys Glu Lys Lys Glu Lys Lys Glu Arg Met Ser Ala Ala Glu
20 25 30

Leu Arg Ser Leu Glu Glu Met Ser Leu Arg Arg Gly Phe Phe Asn Leu
35 40 45

Asn Arg Ser Ser Lys Arg Glu Ser Lys Thr Arg Leu Glu Ile Ser Asn
50 55 60

Pro Ile Pro Ile Lys Val Ala Ser Gly Ser Asp Leu His Leu Thr Asp
65 70 75 80

Ile Asp Ser Asp Ser Asn Arg Gly Ser Val Ile Leu Asp Ser Gly His
85 90 95

Leu Ser Thr Ala Ser Ser Ser Asp Asp Leu Lys Gly Glu Glu Gly Ser
100 105 110

Phe Arg Gly Ser Val Leu Gln Arg Ala Ala Lys Phe Gly Ser Leu Ala
115 120 125

Lys Gln Asn Ser Gln Met Ile Val Lys Arg Phe Ser Phe Ser Gln Arg
130 135 140

Ser Arg Asp Glu Ser Ala Ser Glu Thr Ser Thr Pro Ser Glu His Ser
145 150 155 160

Ala Ala Pro Ser Pro Gln Val Glu Val Arg Thr Leu Glu Gly Gln Leu
165 170 175

Val Gln His Pro Gly Pro Gly Ile Pro Arg Pro Gly His Arg Ser Arg
180 185 190

Ala Pro Glu Leu Val Thr Lys Lys Phe Pro Val Asp Leu Arg Leu Pro
195 200 205

Pro Val Val Pro Leu Pro Pro Pro Thr Leu Arg Glu Leu Glu Leu Gln
210 215 220

Arg Arg Pro Thr Gly Asp Phe Gly Phe Ser Leu Arg Arg Thr Thr Met
225 230 235 240

Leu Asp Arg Gly Pro Glu Gly Gln Ala Cys Arg Arg Val Val His Phe
245 250 255

Ala Glu Pro Gly Ala Gly Thr Lys Asp Leu Ala Leu Gly Leu Val Pro
260 265 270

Gly Asp Arg Leu Val Glu Ile Asn Gly His Asn Val Glu Ser Lys Ser
275 280 285

Arg Asp Glu Ile Val Glu Met Ile Arg Gln Ser Gly Asp Ser Val Arg
290 295 300

Leu Lys Val Gln Pro Ile Pro Glu Leu Ser Glu Leu Ser Arg Ser Trp
305 310 315 320

Leu Arg Ser Gly Glu Gly Pro Arg Arg Glu Pro Ser Asp Ala Lys Thr
325 330 335

Glu Glu Gln Ile Ala Ala Glu Glu Ala Trp Asn Glu Thr Glu Lys Val
340 345 350

Trp Leu Val His Arg Asp Gly Phe Ser Leu Ala Ser Gln Leu Lys Ser
355 360 365

Glu Glu Leu Asn Leu Pro Glu Gly Lys Val Arg Val Lys Leu Asp His
370 375 380

Asp Gly Ala Ile Leu Asp Val Asp Glu Asp Asp Val Glu Lys Ala Asn
385 390 395 400

Ala Pro Ser Cys Asp Arg Leu Glu Asp Leu Ala Ser Leu Val Tyr Leu
405 410 415

Asn Glu Ser Ser Val Leu His Thr Leu Arg Gln Arg Tyr Gly Ala Ser
420 425 430

Leu Leu His Thr Tyr Ala Gly Pro Ser Leu Leu Val Leu Gly Pro Arg
435 440 445

Gly Ala Pro Ala Val Tyr Ser Glu Lys Val Met His Met Phe Lys Gly
450 455 460

Cys Arg Arg Glu Asp Met Ala Pro His Ile Tyr Ala Val Ala Gln Thr
465 470 475 480

Ala Tyr Arg Ala Met Leu Met Ser Arg Gln Asp Gln Ser Ile Ile Leu
485 490 495

Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Ser Cys Gln His Leu Val
500 505 510

Gln Tyr Leu Ala Thr Ile Ala Gly Ile Ser Gly Asn Lys Val Phe Ser
515 520 525

Val Glu Lys Trp Gln Ala Leu Tyr Thr Leu Leu Glu Ala Phe Gly Asn
530 535 540

Ser Pro Thr Ile Ile Asn Gly Asn Ala Thr Arg Phe Ser Gln Ile Leu
545 550 555 560

Ser Leu Asp Phe Asp Gln Ala Gly Gln Val Ala Ser Ala Ser Ile Gln
565 570 575

Thr Met Leu Leu Glu Lys Leu Arg Val Ala Arg Arg Pro Ala Ser Glu
580 585 590

Ala Thr Phe Asn Val Phe Tyr Tyr Leu Leu Ala Cys Gly Asp Gly Thr
595 600 605

Leu Arg Thr Glu Leu His Leu Asn His Leu Ala Glu Asn Asn Val Phe
610 615 620

Gly Ile Val Pro Leu Ala Lys Pro Glu Glu Lys Gln Lys Ala Ala Gln
625 630 635 640

Gln Phe Ser Lys Leu Gln Ala Ala Met Lys Val Leu Gly Ile Ser Pro
645 650 655

Asp Glu Gln Lys Ala Cys Trp Phe Ile Leu Ala Ala Ile Tyr His Leu
660 665 670

Gly Ala Ala Gly Ala Thr Lys Glu Ala Ala Glu Ala Gly Arg Lys Gln
675 680 685

Phe Ala Arg His Glu Trp Ala Gln Lys Ala Ala Tyr Leu Leu Gly Cys
690 695 700

Ser Leu Glu Glu Leu Ser Ser Ala Ile Phe Lys His Gln His Lys Gly
705 710 715 720

Gly Thr Leu Gln Arg Ser Thr Ser Phe Arg Gln Gly Pro Glu Glu Ser
725 730 735

Gly Leu Gly Asp Gly Thr Gly Pro Lys Leu Ser Ala Leu Glu Cys Leu
740 745 750

Glu Gly Met Ala Ala Gly Leu Tyr Ser Glu Leu Phe Thr Leu Leu Val
755 760 765

Ser Leu Val Asn Arg Ala Leu Lys Ser Ser Gln His Ser Leu Cys Ser
770 775 780

Met Met Ile Val Asp Thr Pro Gly Phe Gln Asn Pro Glu Gln Gly Gly
785 790 795 800

Ser Ala Arg Gly Ala Ser Phe Glu Glu Leu Cys His Asn Tyr Thr Gln
805 810 815

Asp Arg Leu Gln Arg Leu Phe His Glu Arg Thr Phe Val Gln Glu Leu
820 825 830

Glu Arg Tyr Lys Glu Glu Asn Ile Glu Leu Ala Phe Asp Asp Leu Glu
835 840 845

Pro Pro Thr Asp Asp Ser Val Ala Ala Val Asp Gln Ala Ser His Gln
850 855 860

Ser Leu Val Arg Ser Leu Ala Arg Thr Asp Glu Ala Arg Gly Leu Leu
865 870 875 880

Trp Leu Leu Glu Glu Glu Ala Leu Val Pro Gly Ala Ser Glu Asp Thr
885 890 895

Leu Leu Glu Arg Leu Phe Ser Tyr Tyr Gly Pro Gln Glu Gly Asp Lys
900 905 910

Lys Gly Gln Ser Pro Leu Leu His Ser Ser Lys Pro His His Phe Leu
915 920 925

Leu Gly His Ser His Gly Thr Asn Trp Val Glu Tyr Asn Val Thr Gly
930 935 940

Trp Leu Asn Tyr Thr Lys Gln Asn Pro Ala Thr Gln Asn Ala Pro Arg
945 950 955 960

Leu Leu Gln Asp Ser Gln Lys Lys Ile Ile Ser Asn Leu Phe Leu Gly
965 970 975

Arg Ala Gly Ser Ala Thr Val Leu Ser Gly Ser Ile Ala Gly Leu Glu
980 985 990

Gly Gly Ser Gln Leu Ala Leu Arg Arg Ala Thr Ser Met Arg Lys Thr
995 1000 1005

Phe Thr Thr Gly Met Ala Ala Val Lys Lys Lys Ser Leu Cys Ile
1010 1015 1020

Gln Met Lys Leu Gln Val Asp Ala Leu Ile Asp Thr Ile Lys Lys
1025 1030 1035

Ser Lys Leu His Phe Val His Cys Phe Leu Pro Val Ala Glu Gly
1040 1045 1050

Trp Ala Gly Glu Pro Arg Ser Ala Ser Ser Arg Arg Val Ser Ser
1055 1060 1065

Ser Ser Glu Leu Asp Leu Pro Ser Gly Asp His Cys Glu Ala Gly

1070	1075	1080
Leu Leu Gln Leu Asp Val 1085	Pro Leu Leu Arg Thr 1090	Gln Leu Arg Gly 1095
Ser Arg Leu Leu Asp Ala Met 1100	Arg Met Tyr Arg 1105	Gln Gly Tyr Pro 1110
Asp His Met Val Phe Ser 1115	Glu Phe Arg Arg Arg 1120	Phe Asp Val Leu 1125
Ala Pro His Leu Thr Lys Lys 1130	His Gly Arg Asn Tyr 1135	Ile Val Val 1140
Asp Glu Arg Arg Ala Val 1145	Glu Glu Leu Leu Glu 1150	Cys Leu Asp Leu 1155
Glu Lys Ser Ser Cys Cys Met 1160	Gly Leu Ser Arg 1165	Val Phe Phe Arg 1170
Ala Gly Thr Leu Ala Arg 1175	Leu Glu Glu Gln Arg 1180	Asp Glu Gln Thr 1185
Ser Arg Asn Leu Thr Leu 1190	Phe Gln Ala Ala Cys 1195	Arg Gly Tyr Leu 1200
Ala Arg Gln His Phe Lys Lys 1205	Arg Lys Ile Gln 1210	Asp Leu Ala Ile 1215
Arg Cys Val Gln Lys Asn Ile 1220	Lys Lys Asn Lys 1225	Gly Val Lys Asp 1230
Trp Pro Trp Trp Lys Leu Phe 1235	Thr Thr Val Arg 1240	Pro Leu Ile Glu 1245
Val Gln Leu Ser Glu Glu Gln 1250	Ile Arg Asn Lys 1255	Asp Glu Glu Ile 1260
Gln Gln Leu Arg Ser Lys Leu 1265	Glu Lys Ala Glu 1270	Lys Glu Arg Asn 1275
Glu Leu Arg Leu Asn Ser Asp 1280	Arg Leu Glu Ser 1285	Arg Ile Ser Glu 1290
Leu Thr Ser Glu Leu Thr 1295	Asp Glu Arg Asn Thr 1300	Gly Glu Ser Ala 1305
Ser Gln Leu Leu Asp Ala Glu 1310	Thr Ala Glu Arg 1315	Leu Arg Ala Glu 1320
Lys Glu Met Lys Glu Leu Gln 1325	Thr Gln Tyr Asp 1330	Ala Leu Lys Lys 1335
Gln Met Glu Val Met Glu Met 1340	Glu Val Met Glu 1345	Ala Arg Leu Ile 1350
Arg Ala Ala Glu Ile Asn Gly 1355	Glu Val Asp Asp 1360	Asp Asp Ala Gly 1365

Gly Glu Trp Arg Leu Lys Tyr Glu Arg Ala Val Arg Glu Val Asp
1370 1375 1380

Phe Thr Lys Lys Arg Leu Gln Gln Glu Phe Glu Asp Lys Leu Glu
1385 1390 1395

Val Glu Gln Gln Asn Lys Arg Gln Leu Glu Arg Arg Leu Gly Asp
1400 1405 1410

Leu Gln Ala Asp Ser Glu Glu Ser Gln Arg Ala Leu Gln Gln Leu
1415 1420 1425

Lys Lys Lys Cys Gln Arg Leu Thr Ala Glu Leu Gln Asp Thr Lys
1430 1435 1440

Leu His Leu Glu Gly Gln Gln Val Arg Asn His Glu Leu Glu Lys
1445 1450 1455

Lys Gln Arg Arg Phe Asp Ser Glu Leu Ser Gln Ala His Glu Glu
1460 1465 1470

Ala Gln Arg Glu Lys Leu Gln Arg Glu Lys Leu Gln Arg Glu Lys
1475 1480 1485

Asp Met Leu Leu Ala Glu Ala Phe Ser Leu Lys Gln Gln Leu Glu
1490 1495 1500

Glu Lys Asp Met Asp Ile Ala Gly Phe Thr Gln Lys Val Val Ser
1505 1510 1515

Leu Glu Ala Glu Leu Gln Asp Ile Ser Ser Gln Glu Ser Lys Asp
1520 1525 1530

Glu Ala Ser Leu Ala Lys Val Lys Lys Gln Leu Arg Asp Leu Glu
1535 1540 1545

Ala Lys Val Lys Asp Gln Glu Glu Glu Leu Asp Glu Gln Ala Gly
1550 1555 1560

Thr Ile Gln Met Leu Glu Gln Ala Lys Leu Arg Leu Glu Met Glu
1565 1570 1575

Met Glu Arg Met Arg Gln Thr His Ser Lys Glu Met Glu Ser Arg
1580 1585 1590

Asp Glu Glu Val Glu Glu Ala Arg Gln Ser Cys Gln Lys Lys Leu
1595 1600 1605

Lys Gln Met Glu Val Gln Leu Glu Glu Glu Tyr Glu Asp Lys Gln
1610 1615 1620

Lys Val Leu Arg Glu Lys Arg Glu Leu Glu Gly Lys Leu Ala Thr
1625 1630 1635

Leu Ser Asp Gln Val Asn Arg Arg Asp Phe Glu Ser Glu Lys Arg
1640 1645 1650

Leu Arg Lys Asp Leu Lys Arg Thr Lys Ala Leu Leu Ala Asp Ala
 1655 1660 1665
 Gln Leu Met Leu Asp His Leu Lys Asn Ser Ala Pro Ser Lys Arg
 1670 1675 1680
 Glu Ile Ala Gln Leu Lys Asn Gln Leu Glu Glu Gln Leu Ser Arg
 1685 1690 1695
 Leu Gln Arg Glu Lys Asn Glu Ile Gln Asn Arg Leu Glu Glu Asp
 1700 1705 1710
 Gln Glu Asp Met Asn Glu Leu Met Lys Lys His Lys Ala Ala Val
 1715 1720 1725
 Ala Gln Ala Ser Arg Asp Leu Ala Gln Ile Asn Asp Leu Gln Ala
 1730 1735 1740
 Gln Leu Glu Glu Ala Asn Lys Glu Lys Gln Glu Leu Gln Glu Lys
 1745 1750 1755
 Leu Gln Ala Leu Gln Ser Gln Val Glu Phe Leu Glu Gln Ser Met
 1760 1765 1770
 Val Asp Lys Ser Leu Val Ser Arg Gln Glu Ala Lys Ile Arg Glu
 1775 1780 1785
 Leu Glu Thr Arg Leu Glu Phe Glu Arg Thr Gln Val Lys Arg Leu
 1790 1795 1800
 Glu Ser Leu Ala Ser Arg Leu Lys Glu Asn Met Glu Lys Leu Thr
 1805 1810 1815
 Glu Glu Arg Asp Gln Arg Ile Ala Ala Glu Asn Arg Glu Lys Glu
 1820 1825 1830
 Gln Asn Lys Arg Leu Gln Arg Gln Leu Arg Asp Thr Lys Glu Glu
 1835 1840 1845
 Met Gly Glu Leu Ala Arg Lys Glu Ala Glu Ala Ser Arg Lys Lys
 1850 1855 1860
 His Glu Leu Glu Met Asp Leu Glu Ser Leu Glu Ala Ala Asn Gln
 1865 1870 1875
 Ser Leu Gln Ala Asp Leu Lys Leu Ala Phe Lys Arg Ile Gly Asp
 1880 1885 1890
 Leu Gln Ala Ala Ile Glu Asp Glu Met Glu Ser Asp Glu Asn Glu
 1895 1900 1905
 Asp Leu Ile Asn Ser Leu Gln Asp Met Val Thr Lys Tyr Gln Lys
 1910 1915 1920
 Arg Lys Asn Lys Leu Glu Gly Asp Ser Asp Val Asp Ser Glu Leu
 1925 1930 1935

Glu Asp Arg Val Asp Gly Val Lys Ser Trp Leu Ser Lys Asn Lys
1940 1945 1950

Gly Pro Ser Lys Ala Ala Ser Asp Asp Gly Ser Leu Lys Ser Ser
1955 1960 1965

Ser Pro Thr Ser Tyr Trp Lys Ser Leu Ala Pro Asp Arg Ser Asp
1970 1975 1980

Asp Glu His Asp Pro Leu Asp Asn Thr Ser Arg Pro Arg Tyr Ser
1985 1990 1995

His Ser Tyr Leu Ser Asp Ser Asp Thr Glu Ala Lys Leu Thr Glu
2000 2005 2010

Thr Asn Ala
2015

<210> 178

<211> S22

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 178

Met Thr Leu Leu Trp Cys Val Val Ser Leu Tyr Phe Tyr Gly Ile Leu
1 5 10 15

Gln Ser Asp Ala Ser Glu Arg Cys Asp Asp Trp Gly Leu Asp Thr Met
20 25 30

Arg Gln Ile Gln Val Phe Glu Asp Glu Pro Ala Arg Ile Lys Cys Pro
35 40 45

Leu Phe Glu His Phe Leu Lys Phe Asn Tyr Ser Thr Ala His Ser Ala
50 55 60

Gly Leu Thr Leu Ile Trp Tyr Trp Thr Arg Gln Asp Arg Asp Leu Glu
65 70 75 80

Glu Pro Ile Asn Phe Arg Leu Pro Glu Asn Arg Ile Ser Lys Glu Lys
85 90 95

Asp Val Leu Trp Phe Arg Pro Thr Leu Leu Asn Asp Thr Gly Asn Tyr
100 105 110

Thr Cys Met Leu Arg Asn Thr Thr Tyr Cys Ser Lys Val Ala Phe Pro
115 120 125

Leu Glu Val Val Gln Lys Asp Ser Cys Phe Asn Ser Pro Met Lys Leu
130 135 140

Pro Val His Lys Leu Tyr Ile Glu Tyr Gly Ile Gln Arg Ile Thr Cys
145 150 155 160

Pro Asn Val Asp Gly Tyr Phe Pro Ser Ser Val Lys Pro Thr Ile Thr
165 170 175

Trp Tyr Met Gly Cys Tyr Lys Ile Gln Asn Phe Asn Asn Val Ile Pro
 180 185 190
 Glu Gly Met Asn Leu Ser Phe Leu Ile Ala Leu Ile Ser Asn Asn Gly
 195 200 205
 Asn Tyr Thr Cys Val Val Thr Tyr Pro Glu Asn Gly Arg Thr Phe His
 210 215 220
 Leu Thr Arg Thr Leu Thr Val Lys Val Val Gly Ser Pro Lys Asn Ala
 225 230 235 240
 Val Pro Pro Val Ile His Ser Pro Asn Asp His Val Val Tyr Glu Lys
 245 250 255
 Glu Pro Gly Glu Glu Leu Leu Ile Pro Cys Thr Val Tyr Phe Ser Phe
 260 265 270
 Leu Met Asp Ser Arg Asn Glu Val Trp Trp Thr Ile Asp Gly Lys Lys
 275 280 285
 Pro Asp Asp Ile Thr Ile Asp Val Thr Ile Asn Glu Ser Ile Ser His
 290 295 300
 Ser Arg Thr Glu Asp Glu Thr Arg Thr Gln Ile Leu Ser Ile Lys Lys
 305 310 315 320
 Val Thr Ser Glu Asp Leu Lys Arg Ser Tyr Val Cys His Ala Arg Ser
 325 330 335
 Ala Lys Gly Glu Val Ala Lys Ala Ala Lys Val Lys Gln Lys Val Pro
 340 345 350
 Ala Pro Arg Tyr Thr Val Glu Leu Ala Cys Gly Phe Gly Ala Thr Val
 355 360 365
 Leu Leu Val Val Ile Leu Ile Val Val Tyr His Val Tyr Trp Leu Glu
 370 375 380
 Met Val Leu Phe Tyr Arg Ala His Phe Gly Thr Asp Glu Thr Ile Leu
 385 390 395 400
 Val Val Thr Asp Glu Thr Leu Ser Phe Ile Gln Lys Ser Arg Arg Leu
 405 410 415
 Leu Val Val Leu Ser Pro Asn Tyr Val Leu Gln Gly Thr Gln Ala Leu
 420 425 430
 Leu Glu Leu Lys Ala Gly Leu Glu Asn Met Ala Ser Arg Gly Asn Ile
 435 440 445
 Asn Val Ile Leu Val Gln Tyr Lys Ala Val Lys Glu Thr Lys Val Lys
 450 455 460
 Glu Leu Lys Arg Ala Lys Thr Val Leu Thr Val Ile Lys Trp Lys Gly
 465 470 475 480

Glu Lys Ser Lys Tyr Pro Gln Gly Arg Phe Trp Lys Gln Leu Gln Val
485 490 495

Ala Met Pro Val Lys Lys Ser Pro Arg Arg Ser Ser Ser Asp Glu Gln
500 505 510

Gly Leu Ser Tyr Ser Ser Leu Lys Asn Val
515 520

<210> 179

<211> 140

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<220>

<221> misc feature

<222> (21)..(21)

<223> Xaa can be any naturally occurring amino acid

<400> 179

Met Lys Ala Pro Ile Pro His Leu Ile Leu Leu Tyr Ala Thr Phe Thr
1 5 10 15

Gln Ser Leu Lys Xaa Val Thr Lys Arg Gly Ser Ala Asp Gly Cys Thr
20 25 30

Asp Trp Ser Ile Asp Ile Lys Lys Tyr Gln Val Leu Val Gly Glu Pro
35 40 45

Val Arg Ile Lys Cys Ala Leu Phe Tyr Gly Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Leu Ala Gln Ser Ala Gly Leu Ser Leu Met Trp Tyr Lys Ser Ser
65 70 75 80

Gly Pro Gly Asp Phe Glu Glu Pro Ile Ala Phe Asp Gly Ser Arg Met
85 90 95

Ser Lys Glu Glu Asp Ser Ile Trp Phe Arg Pro Thr Leu Leu Gln Asp
100 105 110

Ser Gly Leu Tyr Ala Cys Val Ile Arg Asn Ala Gly Gln Lys His Gly
115 120 125

Gly Gln Val Leu Tyr Ser Lys Glu Ile Leu Cys Leu
130 135 140

<210> 180

<211> 185

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<220>

<221> misc feature

<222> (21)..(21)

<223> Xaa can be any naturally occurring amino acid

<400> 180

Met Lys Ala Pro Ile Pro His Leu Ile Leu Leu Tyr Ala Thr Phe Thr
 1 5 10 15

Gln Ser Leu Lys Xaa Val Thr Lys Arg Gly Ser Ala Asp Gly Cys Thr
 20 25 30

Asp Trp Ser Ile Asp Ile Lys Lys Tyr Gln Val Leu Val Gly Glu Pro
 35 40 45

Val Arg Ile Lys Cys Ala Leu Phe Tyr Gly Tyr Ile Arg Thr Asn Tyr
 50 55 60

Ser Leu Ala Gln Ser Ala Gly Leu Ser Leu Met Trp Tyr Lys Ser Ser
 65 70 75 80

Gly Pro Gly Asp Phe Glu Glu Pro Ile Ala Phe Asp Gly Ser Arg Met
 85 90 95

Ser Lys Glu Glu Asp Ser Ile Trp Phe Arg Pro Thr Leu Leu Gln Asp
 100 105 110

Ser Gly Leu Tyr Ala Cys Val Ile Arg Asn Ser Thr Tyr Cys Met Lys
 115 120 125

Val Ser Ile Ser Leu Thr Val Gly Glu Asn Asp Thr Gly Leu Cys Tyr
 130 135 140

Asn Ser Lys Met Lys Tyr Phe Glu Lys Ala Glu Leu Ser Lys Ser Lys
 145 150 155 160

Glu Ile Ser Cys Arg Asp Ile Glu Asp Phe Leu Leu Pro Thr Arg Glu
 165 170 175

Pro Glu Ile Leu Trp Tyr Lys Pro Leu
 180 185

<210> 181

<211> 671

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<220>

<221> misc feature

<222> (21), (21)

<223> Xaa can be any naturally occurring amino acid

<400> 181

Met Lys Ala Pro Ile Pro His Leu Ile Leu Leu Tyr Ala Thr Phe Thr
 1 5 10 15

Gln Ser Leu Lys Xaa Val Thr Lys Arg Gly Ser Ala Asp Gly Cys Thr
 20 25 30

Asp Trp Ser Ile Asp Ile Lys Lys Tyr Gln Val Leu Val Gly Glu Pro
 35 40 45

Val Arg Ile Lys Cys Ala Leu Phe Tyr Gly Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Leu Ala Gln Ser Ala Gly Leu Ser Leu Met Trp Tyr Lys Ser Ser
65 70 75 80

Gly Pro Gly Asp Phe Glu Glu Pro Ile Ala Phe Asp Gly Ser Arg Met
85 90 95

Ser Lys Glu Glu Asp Ser Ile Trp Phe Arg Pro Thr Leu Leu Gln Asp
100 105 110

Ser Gly Leu Tyr Ala Cys Val Ile Arg Asn Ser Thr Tyr Cys Met Lys
115 120 125

Val Ser Ile Ser Leu Thr Val Gly Glu Asn Asp Thr Gly Leu Cys Tyr
130 135 140

Asn Ser Lys Met Lys Tyr Phe Glu Lys Ala Glu Leu Ser Lys Ser Lys
145 150 155 160

Glu Ile Ser Cys Arg Asp Ile Glu Asp Phe Leu Leu Pro Thr Arg Glu
165 170 175

Pro Glu Ile Leu Trp Tyr Lys Glu Cys Arg Thr Lys Thr Trp Arg Pro
180 185 190

Ser Ile Val Phe Lys Arg Asp Thr Leu Leu Ile Arg Glu Val Arg Glu
195 200 205

Asp Asp Ile Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Gly Gly Phe Val
210 215 220

Val Arg Arg Thr Thr Glu Leu Thr Val Thr Gly Asp Ser Ala Asn Leu
225 230 235 240

Thr Cys Arg Ala Phe Phe Gly Tyr Ser Gly Asp Val Ser Pro Leu Ile
245 250 255

Tyr Trp Met Lys Gly Glu Lys Phe Ile Glu Asp Leu Asp Glu Asn Arg
260 265 270

Val Trp Glu Ser Asp Ile Arg Ile Leu Lys Glu His Leu Gly Glu Gln
275 280 285

Glu Val Ser Ile Ser Leu Ile Val Asp Ser Val Glu Glu Gly Asp Leu
290 295 300

Gly Asn Tyr Ser Cys Tyr Val Glu Asn Gly Asn Gly Arg Arg His Ala
305 310 315 320

Ser Val Leu Leu His Lys Arg Glu Leu Met Tyr Thr Val Glu Leu Ala
325 330 335

Gly Gly Leu Gly Ala Ile Leu Leu Leu Leu Val Cys Leu Val Thr Ile
340 345 350

Tyr Lys Cys Tyr Lys Ile Glu Ile Met Leu Phe Tyr Arg Asn His Phe
355 360 365

Gly Ala Glu Glu Leu Asp Gly Asp Asn Lys Asp Tyr Asp Ala Tyr Leu
370 375 380

Ser Tyr Thr Lys Val Asp Pro Asp Gln Trp Asn Gln Glu Thr Gly Glu
385 390 395 400

Glu Glu Arg Phe Ala Leu Glu Ile Leu Pro Asp Met Leu Glu Lys His
405 410 415

Tyr Gly Tyr Lys Leu Phe Ile Pro Asp Arg Asp Leu Ile Pro Thr Gly
420 425 430

Thr Tyr Ile Glu Asp Val Ala Arg Cys Val Asp Gln Ser Lys Arg Leu
435 440 445

Ile Ile Val Met Thr Pro Asn Tyr Val Val Arg Arg Gly Trp Ser Ile
450 455 460

Phe Glu Leu Glu Thr Arg Leu Arg Asn Met Leu Val Thr Gly Glu Ile
465 470 475 480

Lys Val Ile Leu Ile Glu Cys Ser Glu Leu Arg Gly Ile Met Asn Tyr
485 490 495

Gln Glu Val Glu Ala Leu Lys His Thr Ile Lys Leu Leu Thr Val Ile
500 505 510

Lys Trp His Gly Pro Lys Cys Asn Lys Leu Asn Ser Lys Phe Trp Lys
515 520 525

Arg Leu Gln Tyr Glu Met Pro Phe Lys Arg Ile Glu Pro Ile Thr His
530 535 540

Glu Gln Ala Leu Asp Val Ser Glu Gln Gly Pro Phe Gly Glu Leu Gln
545 550 555 560

Thr Val Ser Ala Ile Ser Met Ala Ala Thr Ser Thr Ala Leu Ala
565 570 575

Thr Ala His Pro Asp Leu Arg Ser Thr Phe His Asn Thr Tyr His Ser
580 585 590

Gln Met Arg Gln Lys His Tyr Tyr Arg Ser Tyr Glu Tyr Asp Val Pro
595 600 605

Pro Thr Gly Thr Leu Pro Leu Thr Ser Ile Gly Asn Gln His Thr Tyr
610 615 620

Cys Asn Ile Pro Met Thr Leu Ile Asn Gly Gln Arg Pro Gln Thr Lys
625 630 635 640

Ser Ser Arg Glu Gln Asn Pro Asp Glu Ala His Thr Asn Ser Ala Ile
645 650 655

Leu Pro Leu Leu Pro Arg Glu Thr Ser Ile Ser Ser Val Ile Trp
 660 665 670

<210> 182

<211> 274

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<220>

<221> misc_feature

<222> (21)..(21)

<223> Xaa can be any naturally occurring amino acid

<400> 182

Met Lys Ala Pro Ile Pro His Leu Ile Leu Leu Tyr Ala Thr Phe Thr
 1 5 10 15

Gln Ser Leu Lys Xaa Val Thr Lys Arg Gly Ser Ala Asp Gly Cys Thr
 20 25 30

Asp Trp Ser Ile Asp Ile Lys Lys Tyr Gln Val Leu Val Gly Glu Pro
 35 40 45

Val Arg Ile Lys Cys Ala Leu Phe Tyr Gly Tyr Ile Arg Thr Asn Tyr
 50 55 60

Ser Leu Ala Gln Ser Ala Gly Leu Ser Leu Met Trp Tyr Lys Ser Ser
 65 70 75 80

Gly Pro Gly Asp Phe Glu Glu Pro Ile Ala Phe Asp Gly Ser Arg Met
 85 90 95

Ser Lys Glu Glu Asp Ser Ile Trp Phe Arg Pro Thr Leu Leu Gln Asp
 100 105 110

Ser Gly Leu Tyr Ala Cys Val Ile Arg Asn Ser Thr Tyr Cys Met Lys
 115 120 125

Val Ser Ile Ser Leu Thr Val Gly Glu Asn Asp Thr Gly Leu Cys Tyr
 130 135 140

Asn Ser Lys Met Lys Tyr Phe Glu Lys Ala Glu Leu Ser Lys Ser Lys
 145 150 155 160

Glu Ile Ser Cys Arg Asp Ile Glu Asp Phe Leu Leu Pro Thr Arg Glu
 165 170 175

Pro Glu Ile Leu Trp Tyr Lys Glu Cys Arg Thr Lys Thr Trp Arg Pro
 180 185 190

Ser Ile Val Phe Lys Arg Asp Thr Leu Leu Ile Arg Glu Val Arg Glu
 195 200 205

Asp Asp Ile Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Gly Gly Phe Val
 210 215 220

Val Arg Arg Thr Thr Glu Leu Thr Val Thr Ala Pro Leu Thr Asp Lys

225 230 235 240
Pro Pro Lys Leu Leu Tyr Pro Met Glu Ser Lys Leu Thr Ile Gln Glu
 245 250 255

Thr Gln Leu Glu Phe Leu Arg Ser Ile Leu Gly Asn Arg Lys Phe Pro
 260 265 270

Ser His

<210> 183

<211> 325

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<220>

<221> misc_feature

<222> (21)..(21)

<223> Xaa can be any naturally occurring amino acid

<400> 183

Met Lys Ala Pro Ile Pro His Leu Ile Leu Leu Tyr Ala Thr Phe Thr
1 5 10 15

Gln Ser Leu Lys Xaa Val Thr Lys Arg Gly Ser Ala Asp Gly Cys Thr
 20 25 30

Asp Trp Ser Ile Asp Ile Lys Lys Tyr Gln Val Leu Val Gly Glu Pro
35 40 45

Val Arg Ile Lys Cys Ala Leu Phe Tyr Gly Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Leu Ala Gln Ser Ala Gly Leu Ser Leu Met Trp Tyr Lys Ser Ser
65 70 75 80

Gly Pro Gly Asp Phe Glu Glu Pro Ile Ala Phe Asp Gly Ser Arg Met
 85 90 95

Ser Lys Glu Glu Asp Ser Ile Trp Phe Arg Pro Thr Leu Leu Gln Asp
100 105 110

Ser Gly Leu Tyr Ala Cys Val Ile Arg Asn Ser Thr Tyr Cys Met Lys
115 120 125

Val Ser Ile Ser Leu Thr Val Gly Glu Asn Asp Thr Gly Leu Cys Tyr
130 135 140

Asn Ser Lys Met Lys Tyr Phe Glu Lys Ala Glu Leu Ser Lys Ser Lys
145 150 155 160

Glu Ile Ser Cys Arg Asp Ile Glu Asp Phe Leu Leu Pro Thr Arg Glu
 165 170 175

Pro Glu Ile Leu Trp Tyr Lys Glu Cys Arg Thr Lys Thr Trp Arg Pro
180 185 190

Ser Ile Val Phe Lys Arg Asp Thr Leu Leu Ile Arg Glu Val Arg Glu
195 200 205

Asp Asp Ile Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Gly Gly Phe Val
210 215 220

Val Arg Arg Thr Thr Glu Leu Thr Val Thr Ala Pro Leu Thr Asp Lys
225 230 235 240

Pro Pro Lys Leu Leu Tyr Pro Met Glu Ser Lys Leu Thr Ile Gln Glu
245 250 255

Thr Gln Leu Gly Asp Ser Ala Asn Leu Thr Cys Arg Ala Phe Phe Gly
260 265 270

Tyr Ser Gly Asp Val Ser Pro Leu Ile Tyr Trp Met Lys Gly Glu Lys
275 280 285

Phe Ile Glu Asp Leu Asp Glu Asn Arg Val Trp Glu Ser Asp Ile Arg
290 295 300

Ala Asn Val His Ser Gly Thr Cys Cys Arg Pro Cys Cys Tyr Ser Cys
305 310 315 320

Cys Leu Tyr Val Trp
325

<210> 184

<211> 128

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 184

Met Lys Pro Pro Phe Leu Leu Ala Leu Val Val Cys Ser Val Val Ser
1 5 10 15

Thr Asn Leu Lys Met Val Ser Lys Arg Asn Ser Val Asp Gly Cys Ile
20 25 30

Asp Trp Ser Val Asp Leu Lys Thr Tyr Met Ala Leu Ala Gly Glu Pro
35 40 45

Val Arg Val Lys Cys Ala Leu Phe Tyr Ser Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Thr Ala Gln Ser Thr Gly Leu Arg Leu Met Trp Tyr Lys Asn Lys
65 70 75 80

Gly Asp Leu Glu Glu Pro Ile Ile Phe Ser Glu Val Arg Met Ser Lys
85 90 95

Glu Glu Asp Ser Ile Trp Phe His Ser Ala Glu Ala Gln Asp Ser Gly
100 105 110

Phe Tyr Thr Cys Val Leu Arg Asn Ala Ser Gln Lys Cys Gly Glu Ala

115 120 125

<210> 185
<211> 201
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 185

Met Lys Pro Pro Phe Leu Leu Ala Leu Val Val Cys Ser Val Val Ser
1 5 10 15

Thr Asn Leu Lys Met Val Ser Lys Arg Asn Ser Val Asp Gly Cys Ile
20 25 30

Asp Trp Ser Val Asp Leu Lys Thr Tyr Met Ala Leu Ala Gly Glu Pro
35 40 45

Val Arg Val Lys Cys Ala Leu Phe Tyr Ser Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Thr Ala Gln Ser Thr Gly Leu Arg Leu Met Trp Tyr Lys Asn Lys
65 70 75 80

Gly Asp Leu Glu Glu Pro Ile Ile Phe Ser Glu Val Arg Met Ser Lys
85 90 95

Glu Glu Asp Ser Ile Trp Phe His Ser Ala Glu Ala Gln Asp Ser Gly
100 105 110

Phe Tyr Thr Cys Val Leu Arg Asn Ser Thr Tyr Cys Met Lys Val Ser
115 120 125

Met Ser Leu Thr Val Ala Glu Asn Glu Ser Gly Leu Cys Tyr Asn Ser
130 135 140

Arg Ile Arg Tyr Leu Glu Lys Ser Glu Val Thr Lys Arg Lys Glu Ile
145 150 155 160

Ser Cys Pro Asp Met Asp Asp Phe Lys Lys Ser Asp Gln Glu Pro Asp
165 170 175

Val Val Trp Tyr Lys Leu Tyr Ser Gln Thr Ser Leu Pro Ser His Cys
180 185 190

Ser Pro Trp Arg Ile Ser Gln Val Leu
195 200

<210> 186
<211> 661
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 186

Met Lys Pro Pro Phe Leu Leu Ala Leu Val Val Cys Ser Val Val Ser
1 5 10 15

Thr Asn Leu Lys Met Val Ser Lys Arg Asn Ser Val Asp Gly Cys Ile
 20 25 30
 Asp Trp Ser Val Asp Leu Lys Thr Tyr Met Ala Leu Ala Gly Glu Pro
 35 40 45
 Val Arg Val Lys Cys Ala Leu Phe Tyr Ser Tyr Ile Arg Thr Asn Tyr
 50 55 60
 Ser Thr Ala Gln Ser Thr Gly Leu Arg Leu Met Trp Tyr Lys Asn Lys
 65 70 75 80
 Gly Asp Leu Glu Glu Pro Ile Ile Phe Ser Glu Val Arg Met Ser Lys
 85 90 95
 Glu Glu Asp Ser Ile Trp Phe His Ser Ala Glu Ala Gln Asp Ser Gly
 100 105 110
 Phe Tyr Thr Cys Val Leu Arg Asn Ser Thr Tyr Cys Met Lys Val Ser
 115 120 125
 Met Ser Leu Thr Val Ala Glu Asn Glu Ser Gly Leu Cys Tyr Asn Ser
 130 135 140
 Arg Ile Arg Tyr Leu Glu Lys Ser Glu Val Thr Lys Arg Lys Glu Ile
 145 150 155 160
 Ser Cys Pro Asp Met Asp Asp Phe Lys Lys Ser Asp Gln Glu Pro Asp
 165 170 175
 Val Val Trp Tyr Lys Glu Cys Lys Pro Lys Met Trp Arg Ser Ile Ile
 180 185 190
 Ile Gln Lys Gly Asn Ala Leu Leu Ile Gln Glu Val Gln Glu Glu Asp
 195 200 205
 Gly Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Glu Gly Lys Leu Val Arg
 210 215 220
 Arg Thr Thr Glu Leu Lys Val Thr Gly Lys Pro Leu Asn Ile Pro Cys
 225 230 235 240
 Lys Ala Phe Phe Gly Phe Ser Gly Glu Ser Gly Pro Met Ile Tyr Trp
 245 250 255
 Met Lys Gly Glu Lys Phe Ile Glu Glu Leu Ala Gly His Ile Arg Glu
 260 265 270
 Gly Glu Ile Arg Leu Leu Lys Glu His Leu Gly Glu Lys Glu Val Glu
 275 280 285
 Leu Ala Leu Ile Phe Asp Ser Val Val Glu Ala Asp Leu Ala Asn Tyr
 290 295 300
 Thr Cys His Val Glu Asn Arg Asn Gly Arg Lys His Ala Ser Val Leu
 305 310 315 320

Leu Arg Lys Lys Asp Leu Ile Tyr Lys Ile Glu Leu Ala Gly Gly Leu
325 330 335

Gly Ala Ile Phe Leu Leu Leu Val Leu Leu Val Val Ile Tyr Lys Cys
340 345 350

Tyr Asn Ile Glu Leu Met Leu Phe Tyr Arg Gln His Phe Gly Ala Asp
355 360 365

Glu Thr Asn Asp Asp Asn Lys Glu Tyr Asp Ala Tyr Leu Ser Tyr Thr
370 375 380

Lys Val Asp Gln Asp Thr Leu Asp Cys Asp Asn Pro Glu Glu Glu Gln
385 390 395 400

Phe Ala Leu Glu Val Leu Pro Asp Val Leu Glu Lys His Tyr Gly Tyr
405 410 415

Lys Leu Phe Ile Pro Glu Arg Asp Leu Ile Pro Ser Gly Thr Tyr Met
420 425 430

Glu Asp Leu Thr Arg Tyr Val Glu Gln Ser Arg Arg Leu Ile Ile Val
435 440 445

Leu Thr Pro Asp Tyr Ile Leu Arg Arg Gly Trp Ser Ile Phe Glu Leu
450 455 460

Glu Ser Arg Leu His Asn Met Leu Val Ser Gly Glu Ile Lys Val Ile
465 470 475 480

Leu Ile Glu Cys Thr Glu Leu Lys Gly Lys Val Asn Cys Gln Glu Val
485 490 495

Glu Ser Leu Lys Arg Ser Ile Lys Leu Leu Ser Leu Ile Lys Trp Lys
500 505 510

Gly Ser Lys Ser Ser Lys Leu Asn Ser Lys Phe Trp Lys His Leu Val
515 520 525

Tyr Glu Met Pro Ile Lys Lys Lys Glu Met Leu Pro Arg Cys His Val
530 535 540

Leu Asp Ser Ala Glu Gln Gly Leu Phe Gly Glu Leu Gln Pro Ile Pro
545 550 555 560

Ser Ile Ala Met Thr Ser Thr Ser Ala Thr Leu Val Ser Ser Gln Ala
565 570 575

Asp Leu Pro Glu Phe His Pro Ser Asp Ser Met Gln Ile Arg His Cys
580 585 590

Cys Arg Gly Tyr Lys His Glu Ile Pro Ala Thr Thr Leu Pro Val Pro
595 600 605

Ser Leu Gly Asn His His Thr Tyr Cys Asn Leu Pro Leu Thr Leu Leu
610 615 620

Asn Gly Gln Leu Pro Leu Asn Asn Thr Leu Lys Asp Thr Gln Glu Phe
625 630 635 640

His Arg Asn Ser Ser Leu Leu Pro Leu Ser Ser Lys Glu Leu Ser Phe
645 650 655

Thr Ser Asp Ile Trp
660

<210> 187

<211> 307

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 187

Met Lys Pro Pro Phe Leu Leu Ala Leu Val Val Cys Ser Val Val Ser
1 5 10 15

Thr Asn Leu Lys Met Val Ser Lys Arg Asn Ser Val Asp Gly Cys Ile
20 25 30

Asp Trp Ser Val Asp Leu Lys Thr Tyr Met Ala Leu Ala Gly Glu Pro
35 40 45

Val Arg Val Lys Cys Ala Leu Phe Tyr Ser Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Thr Ala Gln Ser Thr Gly Leu Arg Leu Met Trp Tyr Lys Asn Lys
65 70 75 80

Gly Asp Leu Glu Glu Pro Ile Ile Phe Ser Glu Val Arg Met Ser Lys
85 90 95

Glu Glu Asp Ser Ile Trp Phe His Ser Ala Glu Ala Gln Asp Ser Gly
100 105 110

Phe Tyr Thr Cys Val Leu Arg Asn Ser Thr Tyr Cys Met Lys Val Ser
115 120 125

Met Ser Leu Thr Val Ala Glu Asn Glu Ser Gly Leu Cys Tyr Asn Ser
130 135 140

Arg Ile Arg Tyr Leu Glu Lys Ser Glu Val Thr Lys Arg Lys Glu Ile
145 150 155 160

Ser Cys Pro Asp Met Asp Asp Phe Lys Lys Ser Asp Gln Glu Pro Asp
165 170 175

Val Val Trp Tyr Lys Glu Cys Lys Pro Lys Met Trp Arg Ser Ile Ile
180 185 190

Ile Gln Lys Gly Asn Ala Leu Leu Ile Gln Glu Val Gln Glu Glu Asp
195 200 205

Gly Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Glu Gly Lys Leu Val Arg
210 215 220

Arg Thr Thr Glu Leu Lys Val Thr Ala Leu Leu Thr Asp Lys Pro Pro
225 230 235 240

Lys Pro Leu Phe Pro Met Glu Asn Gln Pro Ser Val Ile Asp Val Gln
245 250 255

Leu Gly Phe Ser Lys Ser Ile Leu Glu Lys Lys Lys Leu Asn Trp His
260 265 270

Ser Ser Leu Thr Gln Leu Trp Lys Leu Thr Trp Arg Ile Ile Pro Ala
275 280 285

Met Leu Lys Thr Glu Met Asp Gly Asn Met Pro Val Phe Cys Cys Val
290 295 300

Lys Arg Ile
305

<210> 188

<211> 304

<212> FRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 188

Met Lys Pro Pro Phe Leu Leu Ala Leu Val Val Cys Ser Val Val Ser
1 5 10 15

Thr Asn Leu Lys Met Val Ser Lys Arg Asn Ser Val Asp Gly Cys Ile
20 25 30

Asp Trp Ser Val Asp Leu Lys Thr Tyr Met Ala Leu Ala Gly Glu Pro
35 40 45

Val Arg Val Lys Cys Ala Leu Phe Tyr Ser Tyr Ile Arg Thr Asn Tyr
50 55 60

Ser Thr Ala Gln Ser Thr Gly Leu Arg Leu Met Trp Tyr Lys Asn Lys
65 70 75 80

Gly Asp Leu Glu Glu Pro Ile Ile Phe Ser Glu Val Arg Met Ser Lys
85 90 95

Glu Glu Asp Ser Ile Trp Phe His Ser Ala Glu Ala Gln Asp Ser Gly
100 105 110

Phe Tyr Thr Cys Val Leu Arg Asn Ser Thr Tyr Cys Met Lys Val Ser
115 120 125

Met Ser Leu Thr Val Ala Glu Asn Glu Ser Gly Leu Cys Tyr Asn Ser
130 135 140

Arg Ile Arg Tyr Leu Glu Lys Ser Glu Val Thr Lys Arg Lys Glu Ile
145 150 155 160

Ser Cys Pro Asp Met Asp Asp Phe Lys Lys Ser Asp Gln Glu Pro Asp
165 170 175

Val Val Trp Tyr Lys Glu Cys Lys Pro Lys Met Trp Arg Ser Ile Ile
180 185 190

Ile Gln Lys Gly Asn Ala Leu Leu Ile Gln Glu Val Gln Glu Glu Asp
195 200 205

Gly Gly Asn Tyr Thr Cys Glu Leu Lys Tyr Glu Gly Lys Leu Val Arg
210 215 220

Arg Thr Thr Glu Leu Lys Val Thr Ala Leu Leu Thr Asp Lys Pro Pro
225 230 235 240

Lys Pro Leu Phe Pro Met Glu Asn Gln Pro Ser Val Ile Asp Val Gln
245 250 255

Leu Gly Lys Pro Leu Asn Ile Pro Cys Lys Ala Phe Phe Gly Phe Ser
260 265 270

Gly Glu Ser Gly Pro Met Ile Tyr Trp Met Lys Gly Glu Lys Phe Ile
275 280 285

Glu Glu Leu Ala Gly His Ile Arg Glu Gly Glu Ile Arg Phe Asn Leu
290 295 300

<210> 189

<211> 221

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 189

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
20 25 30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80

Ala Val Arg Thr Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
85 90 95

Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
100 105 110

Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
115 120 125

Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu

130 135 140
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
145 150 155 160
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
165 170 175
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
180 185 190
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
195 200 205
Gln Leu Pro Val Ser Ser Ser Pro Leu Thr Thr Thr Trp
210 215 220
<210> 190
<211> 417
<212> PRT
<213> Artificial sequence
<220>
<223> A novel predicted alternative spliced variant protein product
<400> 190
Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
1 5 10 15
Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
20 25 30
Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45
Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60
Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80
Ala Val Arg Thr Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
85 90 95
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
100 105 110
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
115 120 125
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
130 135 140
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
145 150 155 160
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
165 170 175

Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
180 185 190

Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
195 200 205

Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
210 215 220

Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
225 230 235 240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
245 250 255

Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
260 265 270

Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
275 280 285

Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
290 295 300

Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
305 310 315 320

Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
325 330 335

Thr Glu Cys His Cys Gln Pro Ala Thr Leu Arg Thr Met Ala Gly Leu
340 345 350

His Gly Pro Ser Gly Pro Pro Val Leu Arg Ala Val Ala Met Glu Phe
355 360 365

Ser Ser Ala Ala Ala Pro Ala Ile Ala Ser Thr Thr Asp Val Arg Ala
370 375 380

Pro Arg Ser Arg His Gly Pro Ala Ile Phe Arg Ser Val Thr Arg Asp
385 390 395 400

Leu Asn Arg Met Val Ala Gly Ala Thr Gly Pro Arg Gly His Leu Val
405 410 415

Leu

<210> 191

<211> 1112

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 191

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
20 25 30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80

Ala Val Arg Thr Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln
85 90 95

Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His
100 105 110

Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu
115 120 125

Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu
130 135 140

Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val
145 150 155 160

Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn
165 170 175

Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala
180 185 190

Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe
195 200 205

Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu
210 215 220

Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu
225 230 235 240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
245 250 255

Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
260 265 270

Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
275 280 285

Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
290 295 300

Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
305 310 315 320

Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
325 330 335

Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
340 345 350

Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
355 360 365

Cys Pro Arg Cys Trp Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser
370 375 380

Pro Trp Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg
385 390 395 400

Ile Arg Leu Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys
405 410 415

Glu Gly Glu Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro
420 425 430

Ile Asn Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val
435 440 445

Thr Cys Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro
450 455 460

Thr Pro Gln Phe Gly Gly Lys Asp Cys Val Gly Asp Val Thr Glu Asn
465 470 475 480

Gln Ile Cys Asn Lys Gln Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn
485 490 495

Pro Cys Phe Ala Gly Val Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp
500 505 510

Lys Cys Gly Ala Cys Pro Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys
515 520 525

Thr Asp Val Asp Glu Cys Lys Glu Val Pro Asp Ala Cys Phe Asn His
530 535 540

Asn Gly Glu His Arg Cys Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu
545 550 555 560

Pro Cys Pro Pro Arg Phe Thr Gly Ser Gln Pro Phe Gly Gln Gly Val
565 570 575

Glu His Ala Thr Ala Asn Lys Gln Val Cys Lys Pro Arg Asn Pro Cys
580 585 590

Thr Asp Gly Thr His Asp Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu
595 600 605

Gly His Tyr Ser Asp Pro Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr
610 615 620

Ala Gly Asn Gly Ile Ile Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp

625 630 635 640

Pro Asn Glu Asn Leu Val Cys Val Ala Asn Ala Thr Tyr His Cys Lys
645 650 655

Lys Asp Asn Cys Pro Asn Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp
660 665 670

Lys Asp Gly Ile Gly Asp Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys
675 680 685

Ile Pro Asp Asp Arg Asp Asn Cys Pro Phe His Tyr Asn Pro Ala Gln
690 695 700

Tyr Asp Tyr Asp Arg Asp Val Gly Asp Arg Cys Asp Asn Cys Pro
705 710 715 720

Tyr Asn His Asn Pro Asp Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly
725 730 735

Asp Ala Cys Ala Ala Asp Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg
740 745 750

Asp Asn Cys Gln Tyr Val Tyr Asn Val Asp Gln Arg Asp Thr Asp Met
755 760 765

Asp Gly Val Gly Asp Gln Cys Asp Asn Cys Pro Leu Glu His Asn Pro
770 775 780

Asp Gln Leu Asp Ser Asp Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn
785 790 795 800

Asn Gln Asp Ile Asp Glu Asp Gly His Gln Asn Asn Leu Asp Asn Cys
805 810 815

Pro Tyr Val Pro Asn Ala Asn Gln Ala Asp His Asp Lys Asp Gly Lys
820 825 830

Gly Asp Ala Cys Asp His Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp
835 840 845

Lys Asp Asn Cys Arg Leu Val Pro Asn Pro Asp Gln Lys Asp Ser Asp
850 855 860

Gly Asp Gly Arg Gly Asp Ala Cys Lys Asp Asp Phe Asp His Asp Ser
865 870 875 880

Val Pro Asp Ile Asp Asp Ile Cys Pro Glu Asn Val Asp Ile Ser Glu
885 890 895

Thr Asp Phe Arg Arg Phe Gln Met Ile Pro Leu Asp Pro Lys Gly Thr
900 905 910

Ser Gln Asn Asp Pro Asn Trp Val Val Arg His Gln Gly Lys Glu Leu
915 920 925

Val Gln Thr Val Asn Cys Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu
930 935 940

Phe Asn Ala Val Asp Phe Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg
945 950 955 960

Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg
965 970 975

Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr
980 985 990

Asn Pro Thr Arg Ala Gln Gly Tyr Ser Gly Leu Ser Val Lys Val Val
995 1000 1005

Asn Ser Thr Thr Gly Pro Gly Glu His Leu Arg Asn Ala Leu Trp
1010 1015 1020

His Thr Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His Asp
1025 1030 1035

Pro Arg His Ile Gly Trp Lys Asp Phe Thr Ala Tyr Arg Trp Arg
1040 1045 1050

Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg Val Val Met Tyr
1055 1060 1065

Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile Tyr Asp Lys
1070 1075 1080

Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu
1085 1090 1095

Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro
1100 1105 1110

<210> 192

<211> 1119

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 192

Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys
1 5 10 15

Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp
20 25 30

Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu
35 40 45

Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala
50 55 60

Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp
65 70 75 80

Ala Val Arg Thr Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln

85	90	95
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His 100 105 110		
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu 115 120 125		
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu 130 135 140		
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val 145 150 155 160		
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn 165 170 175		
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala 180 185 190		
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe 195 200 205		
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu 210 215 220		
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu 225 230 235 240		
Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr 245 250 255		
Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile 260 265 270		
Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg 275 280 285		
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu 290 295 300		
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His 305 310 315 320		
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys 325 330 335		
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser 340 345 350		
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys 355 360 365		
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro 370 375 380		
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln 385 390 395 400		

Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
405 410 415

Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
420 425 430

Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
450 455 460

Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465 470 475 480

Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
485 490 495

Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
500 505 510

Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Thr Pro Gln Phe Gly Gly
515 520 525

Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
530 535 540

Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
545 550 555 560

Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
565 570 575

Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Val
580 585 590

Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn Lys
595 600 605

Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr Arg
610 615 620

Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly Glu
625 630 635 640

Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val Ala
645 650 655

Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro Asn
660 665 670

Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys Asp
675 680 685

Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys Pro
690 695 700

Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val Gly
705 710 715 720

Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala Asp
725 730 735

Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp Gly
740 745 750

Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn Val
755 760 765

Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp Asn
770 775 780

Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp Arg
785 790 795 800

Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly His
805 810 815

Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln Ala
820 825 830

Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp Asp
835 840 845

Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro Asn
850 855 860

Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys Lys
865 870 875 880

Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys Pro
885 890 895

Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met Ile
900 905 910

Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val Val
915 920 925

Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro Gly
930 935 940

Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly Thr
945 950 955 960

Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe
965 970 975

Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val
980 985 990

Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr Ser
995 1000 1005

Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu
1010 1015 1020

His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln
1025 1030 1035

Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp
1040 1045 1050

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly
1055 1060 1065

Phe Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp
1070 1075 1080

Ser Gly Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly
1085 1090 1095

Leu Phe Val Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys
1100 1105 1110

Tyr Glu Cys Arg Asp Pro
1115

<210> 193
<211> 613
<212> PRT
<213> Artificial sequence.

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 193

Met Leu Ala Pro Arg Gly Ala Ala Val Leu Leu Leu His Leu Val Leu
1 5 10 15

Gln Arg Trp Leu Ala Ala Gly Ala Gln Ala Thr Pro Gln Val Phe Asp
20 25 30

Leu Leu Pro Ser Ser Ser Gln Arg Leu Asn Pro Gly Ala Leu Leu Pro
35 40 45

Val Leu Thr Asp Pro Ala Leu Asn Asp Leu Tyr Val Ile Ser Thr Phe
50 55 60

Lys Leu Gln Thr Lys Ser Ser Ala Thr Ile Phe Gly Leu Tyr Ser Ser
65 70 75 80

Thr Asp Asn Ser Lys Tyr Phe Glu Phe Thr Val Met Gly Arg Leu Ser
85 90 95

Lys Ala Ile Leu Arg Tyr Leu Lys Asn Asp Gly Lys Val His Leu Val
100 105 110

Val Phe Asn Asn Leu Gln Leu Ala Asp Gly Arg Arg His Arg Ile Leu
115 120 125

Leu Arg Leu Ser Asn Leu Gln Arg Gly Ala Gly Ser Leu Glu Leu Tyr
130 135 140

Leu Asp Cys Ile Gln Val Asp Ser Val His Asn Leu Pro Arg Ala Phe
 145 150 155 160
 Ala Gly Pro Ser Gln Lys Pro Glu Thr Ile Glu Leu Arg Thr Phe Gln
 165 170 175
 Arg Lys Pro Gln Asp Phe Leu Glu Glu Leu Lys Leu Val Val Arg Gly
 180 185 190
 Ser Leu Phe Gln Val Ala Ser Leu Gln Asp Cys Phe Leu Gln Gln Ser
 195 200 205
 Glu Pro Leu Ala Ala Thr Gly Thr Gly Asp Phe Asn Arg Gln Phe Leu
 210 215 220
 Gly Gln Met Thr Gln Leu Asn Gln Leu Leu Gly Glu Val Lys Asp Leu
 225 230 235 240
 Leu Arg Gln Gln Val Lys Glu Thr Ser Phe Leu Arg Asn Thr Ile Ala
 245 250 255
 Glu Cys Gln Ala Cys Gly Pro Leu Lys Phe Gln Ser Pro Thr Pro Ser
 260 265 270
 Thr Val Val Ala Pro Ala Pro Pro Ala Pro Pro Thr Arg Pro Pro Arg
 275 280 285
 Arg Cys Asp Ser Asn Pro Cys Phe Arg Gly Val Gln Cys Thr Asp Ser
 290 295 300
 Arg Asp Gly Phe Gln Cys Gly Pro Cys Pro Glu Gly Tyr Thr Gly Asn
 305 310 315 320
 Gly Ile Thr Cys Ile Asp Val Asp Glu Cys Lys Tyr His Pro Cys Tyr
 325 330 335
 Pro Gly Val His Cys Ile Asn Leu Ser Pro Gly Phe Arg Cys Asp Ala
 340 345 350
 Cys Pro Val Gly Phe Thr Gly Pro Met Val Gln Gly Val Gly Ile Ser
 355 360 365
 Phe Ala Lys Ser Asn Lys Gln Val Cys Thr Asp Ile Asp Glu Cys Arg
 370 375 380
 Asn Gly Ala Cys Val Pro Asn Ser Ile Cys Val Asn Thr Leu Gly Ser
 385 390 395 400
 Tyr Arg Cys Gly Pro Cys Lys Pro Gly Tyr Thr Gly Asp Gln Ile Arg
 405 410 415
 Gly Cys Lys Val Glu Arg Asn Cys Arg Asn Pro Glu Leu Asn Pro Cys
 420 425 430
 Ser Val Asn Ala Gln Cys Ile Glu Glu Arg Gln Gly Asp Val Thr Cys
 435 440 445

Val Cys Gly Val Gly Trp Ala Gly Asp Gly Tyr Ile Cys Gly Lys Asp
450 455 460

Val Asp Ile Asp Ser Tyr Pro Asp Glu Glu Leu Pro Cys Ser Ala Arg
465 470 475 480

Asn Cys Lys Lys Asp Asn Cys Lys Tyr Val Pro Asn Ser Gly Gln Glu
485 490 495

Asp Ala Asp Arg Asp Gly Ile Gly Asp Ala Cys Asp Glu Asp Ala Asp
500 505 510

Gly Asp Gly Ile Leu Asn Glu Gln Asp Asn Cys Val Leu Ile His Asn
515 520 525

Val Asp Gln Arg Asn Ser Asp Lys Asp Ile Phe Gly Asp Ala Cys Asp
530 535 540

Asn Cys Leu Ser Val Leu Asn Asn Asp Gln Lys Asp Thr Asp Gly Asp
545 550 555 560

Gly Arg Gly Asp Ala Cys Asp Asp Asp Met Asp Gly Asp Gly Ile Lys
565 570 575

Asn Ile Leu Asp Asn Cys Pro Lys Phe Pro Asn Arg Asp Gln Arg Asp
580 585 590

Lys Asp Gly Asp Gly Val Gly Asp Ala Cys Asp Ser Cys Pro Asp Val
595 600 605

Ser Asn Pro Asn Gln
610

<210> 194

<211> 101

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 194

Met Arg Val Leu Gly Gly Arg Cys Gly Ala Leu Leu Ala Cys Leu Leu
1 5 10 15

Leu Val Leu Pro Val Ser Glu Ala Asn Phe Leu Ser Lys Gln Gln Ala
20 25 30

Ser Gln Val Leu Val Arg Lys Arg Arg Ala Asn Ser Leu Leu Glu Glu
35 40 45

Thr Lys Gln Gly Asn Leu Glu Arg Glu Cys Ile Glu Glu Leu Cys Asn
50 55 60

Lys Glu Glu Ala Arg Glu Val Phe Glu Asn Asp Pro Glu Thr Phe Val
65 70 75 80

Phe Ala Leu Phe Lys Leu Gly Tyr Ser Leu Leu His Val Ser Gln Leu
85 90 95

Met Leu Ile Leu Thr
100

<210> 195
<211> 2772
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 195

Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1 5 10 15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
20 25 30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
35 40 45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
50 55 60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65 70 75 80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
85 90 95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
100 105 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
115 120 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
130 135 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145 150 155 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
165 170 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
180 185 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
195 200 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
210 215 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225 230 235 240

Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
245 250 255

Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
260 265 270

Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
275 280 285

Ser Ala Cys Lys Gly Gln Leu Leu Asp Glu Gly Leu Cys Val Glu Ser
290 295 300

Thr Glu Cys Pro Cys Val His Ser Gly Lys Arg Tyr Pro Pro Gly Thr
305 310 315 320

Ser Leu Ser Arg Asp Cys Asn Thr Cys Ile Cys Arg Asn Ser Gln Trp
325 330 335

Ile Cys Ser Asn Glu Glu Cys Pro Gly Glu Cys Leu Val Thr Gly Gln
340 345 350

Ser His Phe Lys Ser Phe Asp Asn Arg Tyr Phe Thr Phe Ser Gly Ile
355 360 365

Cys Gln Tyr Leu Leu Ala Arg Asp Cys Gln Asp His Ser Phe Ser Ile
370 375 380

Val Ile Glu Thr Val Gln Cys Ala Asp Asp Arg Asp Ala Val Cys Thr
385 390 395 400

Arg Ser Val Thr Val Arg Leu Pro Gly Leu His Asn Ser Leu Val Lys
405 410 415

Leu Lys His Gly Ala Gly Val Ala Met Asp Gly Gln Asp Ile Gln Leu
420 425 430

Pro Leu Leu Lys Gly Asp Leu Arg Ile Gln His Thr Val Thr Ala Ser
435 440 445

Val Arg Leu Ser Tyr Gly Glu Asp Leu Gln Met Asp Trp Asp Gly Arg
450 455 460

Gly Arg Leu Leu Val Lys Leu Ser Pro Val Tyr Ala Gly Lys Thr Cys
465 470 475 480

Gly Leu Cys Gly Asn Tyr Asn Gly Asn Gln Gly Asp Asp Phe Leu Thr
485 490 495

Pro Ser Gly Leu Ala Glu Pro Arg Val Glu Asp Phe Gly Asn Ala Trp
500 505 510

Lys Leu His Gly Asp Cys Gln Asp Leu Gln Lys Gln His Ser Asp Pro
515 520 525

Cys Ala Leu Asn Pro Arg Met Thr Arg Phe Ser Glu Glu Ala Cys Ala
530 535 540

Val Leu Thr Ser Pro Thr Phe Glu Ala Cys His Arg Ala Val Ser Pro
545 550 555 560

Leu Pro Tyr Leu Arg Asn Cys Arg Tyr Asp Val Cys Ser Cys Ser Asp
565 570 575

Gly Arg Glu Cys Leu Cys Gly Ala Leu Ala Ser Tyr Ala Ala Ala Cys
580 585 590

Ala Gly Arg Gly Val Arg Val Ala Trp Arg Glu Pro Gly Arg Cys Glu
595 600 605

Leu Asn Cys Pro Lys Gly Gln Val Tyr Leu Gln Cys Gly Thr Pro Cys
610 615 620

Asn Leu Thr Cys Arg Ser Leu Ser Tyr Pro Asp Glu Glu Cys Asn Glu
625 630 635 640

Ala Cys Leu Glu Gly Cys Phe Cys Pro Pro Gly Leu Tyr Met Asp Glu
645 650 655

Arg Gly Asp Cys Val Pro Lys Ala Gln Cys Pro Cys Tyr Tyr Asp Gly
660 665 670

Glu Ile Phe Gln Pro Glu Asp Ile Phe Ser Asp His His Thr Met Cys
675 680 685

Tyr Cys Glu Asp Gly Phe Met His Cys Thr Met Ser Gly Val Pro Gly
690 695 700

Ser Leu Leu Pro Asp Ala Val Leu Ser Ser Pro Leu Ser His Arg Ser
705 710 715 720

Lys Arg Ser Leu Ser Cys Arg Pro Pro Met Val Lys Leu Val Cys Pro
725 730 735

Ala Asp Asn Leu Arg Ala Glu Gly Leu Glu Cys Thr Lys Thr Cys Gln
740 745 750

Asn Tyr Asp Leu Glu Cys Met Ser Met Gly Cys Val Ser Gly Cys Leu
755 760 765

Cys Pro Pro Gly Met Val Arg His Glu Asn Arg Cys Val Ala Leu Glu
770 775 780

Arg Cys Pro Cys Phe His Gln Gly Lys Glu Tyr Ala Pro Gly Glu Thr
785 790 795 800

Val Lys Ile Gly Cys Asn Thr Cys Val Cys Arg Asp Arg Lys Trp Asn
805 810 815

Cys Thr Asp His Val Cys Asp Ala Thr Cys Ser Thr Ile Gly Met Ala
820 825 830

His Tyr Leu Thr Phe Asp Gly Leu Lys Tyr Leu Phe Pro Gly Glu Cys
835 840 845

Gln Tyr Val Leu Val Gln Asp Tyr Cys Gly Ser Asn Pro Gly Thr Phe
850 855 860

Arg Ile Leu Val Gly Asn Lys Gly Cys Ser His Pro Ser Val Lys Cys
865 870 875 880

Lys Lys Arg Val Thr Ile Leu Val Glu Gly Gly Glu Ile Glu Leu Phe
885 890 895

Asp Gly Glu Val Asn Val Lys Arg Pro Met Lys Asp Glu Thr His Phe
900 905 910

Glu Val Val Glu Ser Gly Arg Tyr Ile Ile Leu Leu Leu Gly Lys Ala
915 920 925

Leu Ser Val Val Trp Asp Arg His Leu Ser Ile Ser Val Val Leu Lys
930 935 940

Gln Thr Tyr Gln Glu Lys Val Cys Gly Leu Cys Gly Asn Phe Asp Gly
945 950 955 960

Ile Gln Asn Asn Asp Leu Thr Ser Ser Asn Leu Gln Val Glu Glu Asp
965 970 975

Pro Val Asp Phe Gly Asn Ser Trp Lys Val Ser Ser Gln Cys Ala Asp
980 985 990

Thr Arg Lys Val Pro Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn
995 1000 1005

Ile Met Lys Gln Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr
1010 1015 1020

Ser Asp Val Phe Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro
1025 1030 1035

Tyr Leu Asp Val Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile
1040 1045 1050

Gly Asp Cys Ala Cys Phe Cys Asp Thr Ile Ala Ala Tyr Ala His
1055 1060 1065

Val Cys Ala Gln His Gly Lys Val Val Thr Trp Arg Thr Ala Thr
1070 1075 1080

Leu Cys Pro Gln Ser Cys Glu Glu Arg Asn Leu Arg Glu Asn Gly
1085 1090 1095

Tyr Glu Cys Glu Trp Arg Tyr Asn Ser Cys Ala Pro Ala Cys Gln
1100 1105 1110

Val Thr Cys Gln His Pro Glu Pro Leu Ala Cys Pro Val Gln Cys
1115 1120 1125

Val Glu Gly Cys His Ala His Cys Pro Pro Gly Lys Ile Leu Asp
1130 1135 1140

Glu Leu Leu Gln Thr Cys Val Asp Pro Glu Asp Cys Pro Val Cys
1145 1150 1155

Glu Val Ala Gly Arg Arg Phe Ala Ser Gly Lys Lys Val Thr Leu

1160 1165 1170
 Asn Pro Ser Asp Pro Glu His Cys Gln Ile Cys His Cys Asp Val
 1175 1180 1185
 Val Asn Leu Thr Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu Val
 1190 1195 1200
 Val Pro Pro Thr Asp Ala Pro Val Ser Pro Thr Thr Leu Tyr Val
 1205 1210 1215
 Glu Asp Ile Ser Glu Pro Pro Leu His Asp Phe Tyr Cys Ser Arg
 1220 1225 1230
 Leu Leu Asp Leu Val Phe Leu Leu Asp Gly Ser Ser Arg Leu Ser
 1235 1240 1245
 Glu Ala Glu Phe Glu Val Leu Lys Ala Phe Val Val Asp Met Met
 1250 1255 1260
 Glu Arg Leu Arg Ile Ser Gln Lys Trp Val Arg Val Ala Val Val
 1265 1270 1275
 Glu Tyr His Asp Gly Ser His Ala Tyr Ile Gly Leu Lys Asp Arg
 1280 1285 1290
 Lys Arg Pro Ser Glu Leu Arg Arg Ile Ala Ser Gln Val Lys Tyr
 1295 1300 1305
 Ala Gly Ser Gln Val Ala Ser Thr Ser Glu Val Leu Lys Tyr Thr
 1310 1315 1320
 Leu Phe Gln Ile Phe Ser Lys Ile Asp Arg Pro Glu Ala Ser Arg
 1325 1330 1335
 Ile Ala Leu Leu Leu Met Ala Ser Gln Glu Pro Gln Arg Met Ser
 1340 1345 1350
 Arg Asn Phe Val Arg Tyr Val Gln Gly Leu Lys Lys Lys Lys Val
 1355 1360 1365
 Ile Val Ile Pro Val Gly Ile Gly Pro His Ala Asn Leu Lys Gln
 1370 1375 1380
 Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu Asn Lys Ala Phe Val
 1385 1390 1395
 Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg Asp Glu Ile Val
 1400 1405 1410
 Ser Tyr Leu Cys Asp Leu Ala Pro Glu Ala Pro Pro Pro Thr Leu
 1415 1420 1425
 Pro Pro His Met Ala Gln Val Thr Val Gly Pro Gly Leu Leu Gly
 1430 1435 1440
 Val Ser Thr Leu Gly Pro Lys Arg Asn Ser Met Val Leu Asp Val
 1445 1450 1455

Ala Phe Val Leu Glu Gly Ser Asp Lys Ile Gly Glu Ala Asp Phe
1460 1465 1470

Asn Arg Ser Lys Glu Phe Met Glu Glu Val Ile Gln Arg Met Asp
1475 1480 1485

Val Gly Gln Asp Ser Ile His Val Thr Val Leu Gln Tyr Ser Tyr
1490 1495 1500

Met Val Thr Val Glu Tyr Pro Phe Ser Glu Ala Gln Ser Lys Gly
1505 1510 1515

Asp Ile Leu Gln Arg Val Arg Glu Ile Arg Tyr Gln Gly Gly Asn
1520 1525 1530

Arg Thr Asn Thr Gly Leu Ala Leu Arg Tyr Leu Ser Asp His Ser
1535 1540 1545

Phe Leu Val Ser Gln Gly Asp Arg Glu Gln Ala Pro Asn Leu Val
1550 1555 1560

Tyr Met Val Thr Gly Asn Pro Ala Ser Asp Glu Ile Lys Arg Leu
1565 1570 1575

Pro Gly Asp Ile Gln Val Val Pro Ile Gly Val Gly Pro Asn Ala
1580 1585 1590

Asn Val Gln Glu Leu Glu Arg Ile Gly Trp Pro Asn Ala Pro Ile
1595 1600 1605

Leu Ile Gln Asp Phe Glu Thr Leu Pro Arg Glu Ala Pro Asp Leu
1610 1615 1620

Val Leu Gln Arg Cys Cys Ser Gly Glu Gly Leu Gln Ile Pro Thr
1625 1630 1635

Leu Ser Pro Ala Pro Asp Cys Ser Gln Pro Leu Asp Val Ile Leu
1640 1645 1650

Leu Leu Asp Gly Ser Ser Ser Phe Pro Ala Ser Tyr Phe Asp Glu
1655 1660 1665

Met Lys Ser Phe Ala Lys Ala Phe Ile Ser Lys Ala Asn Ile Gly
1670 1675 1680

Pro Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser Ile Thr
1685 1690 1695

Thr Ile Asp Val Pro Trp Asn Val Val Pro Glu Lys Ala His Leu
1700 1705 1710

Leu Ser Leu Val Asp Val Met Gln Arg Glu Gly Gly Pro Ser Gln
1715 1720 1725

Ile Gly Asp Ala Leu Gly Phe Ala Val Arg Tyr Leu Thr Ser Glu
1730 1735 1740

Met His Gly Ala Arg Pro Gly Ala Ser Lys Ala Val Val Ile Leu
1745 1750 1755

Val Thr Asp Val Ser Val Asp Ser Val Asp Ala Ala Ala Asp Ala
1760 1765 1770

Ala Arg Ser Asn Arg Val Thr Val Phe Pro Ile Gly Ile Gly Asp
1775 1780 1785

Arg Tyr Asp Ala Ala Gln Leu Arg Ile Leu Ala Gly Pro Ala Gly
1790 1795 1800

Asp Ser Asn Val Val Lys Leu Gln Arg Ile Glu Asp Leu Pro Thr
1805 1810 1815

Met Val Thr Leu Gly Asn Ser Phe Leu His Lys Leu Cys Ser Gly
1820 1825 1830

Phe Val Arg Ile Cys Met Asp Glu Asp Gly Asn Glu Lys Arg Pro
1835 1840 1845

Gly Asp Val Trp Thr Leu Pro Asp Gln Cys His Thr Val Thr Cys
1850 1855 1860

Gln Pro Asp Gly Gln Thr Leu Leu Lys Ser His Arg Val Asn Cys
1865 1870 1875

Asp Arg Gly Leu Arg Pro Ser Cys Pro Asn Ser Gln Ser Pro Val
1880 1885 1890

Lys Val Glu Glu Thr Cys Gly Cys Arg Trp Thr Cys Pro Cys Val
1895 1900 1905

Cys Thr Gly Ser Ser Thr Arg His Ile Val Thr Phe Asp Gly Gln
1910 1915 1920

Asn Phe Lys Leu Thr Gly Ser Cys Ser Tyr Val Leu Phe Gln Asn
1925 1930 1935

Lys Glu Gln Asp Leu Glu Val Ile Leu His Asn Gly Ala Cys Ser
1940 1945 1950

Pro Gly Ala Arg Gln Gly Cys Met Lys Ser Ile Glu Val Lys His
1955 1960 1965

Ser Ala Leu Ser Val Glu Leu His Ser Asp Met Glu Val Thr Val
1970 1975 1980

Asn Gly Arg Leu Val Ser Val Pro Tyr Val Gly Gly Asn Met Glu
1985 1990 1995

Val Asn Val Tyr Gly Ala Ile Met His Glu Val Arg Phe Asn His
2000 2005 2010

Leu Gly His Ile Phe Thr Phe Thr Pro Gln Asn Asn Glu Phe Gln
2015 2020 2025

Leu Gln Leu Ser Pro Lys Thr Phe Ala Ser Lys Thr Tyr Gly Leu
 2030 2035 2040
 Cys Gly Ile Cys Asp Glu Asn Gly Ala Asn Asp Phe Met Leu Arg
 2045 2050 2055
 Asp Gly Thr Val Thr Thr Asp Trp Lys Thr Leu Val Gln Glu Trp
 2060 2065 2070
 Thr Val Gln Arg Pro Gly Gln Thr Cys Gln Pro Ile Leu Glu Glu
 2075 2080 2085
 Gln Cys Leu Val Pro Asp Ser Ser His Cys Gln Val Leu Leu Leu
 2090 2095 2100
 Pro Leu Phe Ala Glu Cys His Lys Val Leu Ala Pro Ala Thr Phe
 2105 2110 2115
 Tyr Ala Ile Cys Gln Gln Asp Ser Cys His Gln Glu Gln Val Cys
 2120 2125 2130
 Glu Val Ile Ala Ser Tyr Ala His Leu Cys Arg Thr Asn Gly Val
 2135 2140 2145
 Cys Val Asp Trp Arg Thr Pro Asp Phe Cys Ala Met Ser Cys Pro
 2150 2155 2160
 Pro Ser Leu Val Tyr Asn His Cys Glu His Gly Cys Pro Arg His
 2165 2170 2175
 Cys Asp Gly Asn Val Ser Ser Cys Gly Asp His Pro Ser Glu Gly
 2180 2185 2190
 Cys Phe Cys Pro Pro Asp Lys Val Met Leu Glu Gly Ser Cys Val
 2195 2200 2205
 Pro Glu Glu Ala Cys Thr Gln Cys Ile Gly Glu Asp Gly Val Gln
 2210 2215 2220
 His Gln Phe Leu Glu Ala Trp Val Pro Asp His Gln Pro Cys Gln
 2225 2230 2235
 Ile Cys Thr Cys Leu Ser Gly Arg Lys Val Asn Cys Thr Thr Gln
 2240 2245 2250
 Pro Cys Pro Thr Ala Lys Ala Pro Thr Cys Gly Leu Cys Glu Val
 2255 2260 2265
 Ala Arg Leu Arg Gln Asn Ala Asp Gln Cys Cys Pro Glu Tyr Glu
 2270 2275 2280
 Cys Val Cys Asp Pro Val Ser Cys Asp Leu Pro Pro Val Pro His
 2285 2290 2295
 Cys Glu Arg Gly Leu Gln Pro Thr Leu Thr Asn Pro Gly Glu Cys
 2300 2305 2310
 Arg Pro Asn Phe Thr Cys Ala Cys Arg Lys Glu Glu Cys Lys Arg

2315 2320 2325
Val Ser Pro Pro Ser Cys Pro Pro His Arg Leu Pro Thr Leu Arg
2330 2335 2340
Lys Thr Gln Cys Cys Asp Glu Tyr Glu Cys Ala Cys Asn Cys Val
2345 2350 2355
Asn Ser Thr Val Ser Cys Pro Leu Gly Tyr Leu Ala Ser Thr Ala
2360 2365 2370
Thr Asn Asp Cys Gly Cys Thr Thr Thr Thr Cys Leu Pro Asp Lys
2375 2380 2385
Val Cys Val His Arg Ser Thr Ile Tyr Pro Val Gly Gln Phe Trp
2390 2395 2400
Glu Glu Gly Cys Asp Val Cys Thr Cys Thr Asp Met Glu Asp Ala
2405 2410 2415
Val Met Gly Leu Arg Val Ala Gln Cys Ser Gln Lys Pro Cys Glu
2420 2425 2430
Asp Ser Cys Arg Ser Gly Phe Thr Tyr Val Leu His Glu Gly Glu
2435 2440 2445
Cys Cys Gly Arg Cys Leu Pro Ser Ala Cys Glu Val Val Thr Gly
2450 2455 2460
Ser Pro Arg Gly Asp Ser Gln Ser Ser Trp Lys Ser Val Gly Ser
2465 2470 2475
Gln Trp Ala Ser Pro Glu Asn Pro Cys Leu Ile Asn Glu Cys Val
2480 2485 2490
Arg Val Lys Glu Glu Val Phe Ile Gln Gln Arg Asn Val Ser Cys
2495 2500 2505
Pro Gln Leu Glu Val Pro Val Cys Pro Ser Gly Phe Gln Leu Ser
2510 2515 2520
Cys Lys Thr Ser Ala Cys Cys Pro Ser Cys Arg Cys Glu Arg Met
2525 2530 2535
Glu Ala Cys Met Leu Asn Gly Thr Val Ile Gly Pro Gly Lys Thr
2540 2545 2550
Val Met Ile Asp Val Cys Thr Thr Cys Arg Cys Met Val Gln Val
2555 2560 2565
Gly Val Ile Ser Gly Phe Lys Leu Glu Cys Arg Lys Thr Thr Cys
2570 2575 2580
Asn Pro Cys Pro Leu Gly Tyr Lys Glu Glu Asn Asn Thr Gly Glu
2585 2590 2595
Cys Cys Gly Arg Cys Leu Pro Thr Ala Cys Thr Ile Gln Leu Arg
2600 2605 2610

Gly Gly Gln Ile Met Thr Leu Lys Arg Asp Glu Thr Leu Gln Asp
2615 2620 2625

Gly Cys Asp Thr His Phe Cys Lys Val Asn Glu Arg Gly Glu Tyr
2630 2635 2640

Phe Trp Glu Lys Arg Val Thr Gly Cys Pro Pro Phe Asp Glu His
2645 2650 2655

Lys Cys Leu Ala Glu Gly Gly Lys Ile Met Lys Ile Pro Gly Thr
2660 2665 2670

Cys Cys Asp Thr Cys Glu Glu Pro Glu Cys Asn Asp Ile Thr Ala
2675 2680 2685

Arg Leu Gln Tyr Val Lys Val Gly Ser Cys Lys Ser Glu Val Glu
2690 2695 2700

Val Asp Ile His Tyr Cys Gln Gly Lys Cys Ala Ser Lys Ala Met
2705 2710 2715

Tyr Ser Ile Asp Ile Asn Asp Val Gln Asp Gln Cys Ser Cys Cys
2720 2725 2730

Ser Pro Thr Arg Thr Glu Pro Met Gln Val Ala Leu His Cys Thr
2735 2740 2745

Asn Gly Ser Val Val Tyr His Glu Val Leu Asn Ala Met Glu Cys
2750 2755 2760

Lys Cys Ser Pro Arg Lys Cys Ser Lys
2765 2770

<210> 196

<211> 552

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 196

Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1 5 10 15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
20 25 30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
35 40 45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
50 55 60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65 70 75 80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu

85 90 95
 Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
 100 105 110
 Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
 115 120 125
 Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
 130 135 140
 Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
 145 150 155 160
 Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
 165 170 175
 Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
 180 185 190
 Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
 195 200 205
 Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
 210 215 220
 Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
 225 230 235 240
 Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
 245 250 255
 Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
 260 265 270
 Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
 275 280 285
 Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
 290 295 300
 Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
 305 310 315 320
 Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
 325 330 335
 Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
 340 345 350
 Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
 355 360 365
 Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
 370 375 380
 Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
 385 390 395 400

Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
405 410 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
420 425 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
435 440 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
450 455 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Ala Gly Pro
465 470 475 480

Arg Leu Cys Arg Glu Asp Leu Arg Pro Val Trp Glu Leu Gln Trp Gln
485 490 495

Pro Gly Arg Gly Leu Pro Tyr Pro Leu Trp Ala Gly Gly Ala Pro Gly
500 505 510

Gly Gly Leu Arg Glu Arg Leu Glu Ala Ala Arg Gly Leu Pro Gly Pro
515 520 525

Ala Glu Ala Ala Gln Arg Ser Leu Arg Pro Gln Pro Ala His Glu Gly
530 535 540

Ser Pro Arg Arg Arg Ala Arg Ser
545 550

<210> 197

<211> 2774

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 197

Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1 5 10 15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
20 25 30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
35 40 45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
50 55 60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65 70 75 80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
85 90 95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro

100 105 110
 Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
 115 120 125
 Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
 130 135 140
 Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
 145 150 155 160
 Leu Cys Gly Asp Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
 165 170 175
 Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
 180 185 190
 Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
 195 200 205
 Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
 210 215 220
 Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
 225 230 235 240
 Val Asp Pro Glu Pro Phe Val Ala Leu Cys Glu Lys Thr Leu Cys Glu
 245 250 255
 Cys Ala Gly Gly Leu Glu Cys Ala Cys Pro Ala Leu Leu Glu Tyr Ala
 260 265 270
 Arg Thr Cys Ala Gln Glu Gly Met Val Leu Tyr Gly Trp Thr Asp His
 275 280 285
 Ser Ala Cys Ser Pro Val Cys Pro Ala Gly Met Glu Tyr Arg Gln Cys
 290 295 300
 Val Ser Pro Cys Ala Arg Thr Cys Gln Ser Leu His Ile Asn Glu Met
 305 310 315 320
 Cys Gln Glu Arg Cys Val Asp Gly Cys Ser Cys Pro Glu Gly Gln Leu
 325 330 335
 Leu Asp Glu Gly Leu Cys Val Glu Ser Thr Glu Cys Pro Cys Val His
 340 345 350
 Ser Gly Lys Arg Tyr Pro Pro Gly Thr Ser Leu Ser Arg Asp Cys Asn
 355 360 365
 Thr Cys Ile Cys Arg Asn Ser Gln Trp Ile Cys Ser Asn Glu Glu Cys
 370 375 380
 Pro Gly Glu Cys Leu Val Thr Gly Gln Ser His Phe Lys Ser Phe Asp
 385 390 395 400
 Asn Arg Tyr Phe Thr Phe Ser Gly Ile Cys Gln Tyr Leu Leu Ala Arg
 405 410 415

Asp Cys Gln Asp His Ser Phe Ser Ile Val Ile Glu Thr Val Gln Cys
420 425 430

Ala Asp Asp Arg Asp Ala Val Cys Thr Arg Ser Val Thr Val Arg Leu
435 440 445

Pro Gly Leu His Asn Ser Leu Val Lys Leu Lys His Gly Ala Gly Val
450 455 460

Ala Met Asp Gly Gln Asp Ile Gln Leu Pro Leu Leu Lys Gly Asp Leu
465 470 475 480

Arg Ile Gln His Thr Val Thr Ala Ser Val Arg Leu Ser Tyr Gly Glu
485 490 495

Asp Leu Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu
500 505 510

Ser Pro Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn
515 520 525

Gly Asn Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Ala Glu Pro
530 535 540

Arg Val Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln
545 550 555 560

Asp Leu Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met
565 570 575

Thr Arg Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe
580 585 590

Glu Ala Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys
595 600 605

Arg Tyr Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly
610 615 620

Ala Leu Ala Ser Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val
625 630 635 640

Ala Trp Arg Glu Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln
645 650 655

Val Tyr Leu Gln Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu
660 665 670

Ser Tyr Pro Asp Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe
675 680 685

Cys Pro Pro Gly Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys
690 695 700

Ala Gln Cys Pro Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp
705 710 715 720

Ile Phe Ser Asp His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met
 725 730 735
 His Cys Thr Met Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val
 740 745 750
 Leu Ser Ser Pro Leu Ser His Arg Ser Lys Arg Ser Leu Ser Cys Arg
 755 760 765
 Pro Pro Met Val Lys Leu Val Cys Pro Ala Asp Asn Leu Arg Ala Glu
 770 775 780
 Gly Leu Glu Cys Thr Lys Thr Cys Gln Asn Tyr Asp Leu Glu Cys Met
 785 790 795 800
 Ser Met Gly Cys Val Ser Gly Cys Leu Cys Pro Pro Gly Met Val Arg
 805 810 815
 His Glu Asn Arg Cys Val Ala Leu Glu Arg Cys Pro Cys Phe His Gln
 820 825 830
 Gly Lys Glu Tyr Ala Pro Gly Glu Thr Val Lys Ile Gly Cys Asn Thr
 835 840 845
 Cys Val Cys Arg Asp Arg Lys Trp Asn Cys Thr Asp His Val Cys Asp
 850 855 860
 Ala Thr Cys Ser Thr Ile Gly Met Ala His Tyr Leu Thr Phe Asp Gly
 865 870 875 880
 Leu Lys Tyr Leu Phe Pro Gly Glu Cys Gln Tyr Val Leu Val Gln Asp
 885 890 895
 Tyr Cys Gly Ser Asn Pro Gly Thr Phe Arg Ile Leu Val Gly Asn Lys
 900 905 910
 Gly Cys Ser His Pro Ser Val Lys Cys Lys Lys Arg Val Thr Ile Leu
 915 920 925
 Val Glu Gly Gly Glu Ile Glu Leu Phe Asp Gly Glu Val Asn Val Lys
 930 935 940
 Arg Pro Met Lys Asp Glu Thr His Phe Glu Val Val Glu Ser Gly Arg
 945 950 955 960
 Tyr Ile Ile Leu Leu Leu Gly Lys Ala Leu Ser Val Val Trp Asp Arg
 965 970 975
 His Leu Ser Ile Ser Val Val Leu Lys Gln Thr Tyr Gln Glu Lys Val
 980 985 990
 Cys Gly Leu Cys Gly Asn Phe Asp Gly Ile Gln Asn Asn Asp Leu Thr
 995 1000 1005
 Ser Ser Asn Leu Gln Val Glu Glu Asp Pro Val Asp Phe Gly Asn
 1010 1015 1020

Ser Trp Lys Val Ser Ser Gln Cys Ala Asp Thr Arg Lys Val Pro
 1025 1030 1035
 Leu Asp Ser Ser Pro Ala Thr Cys His Asn Asn Ile Met Lys Gln
 1040 1045 1050
 Thr Met Val Asp Ser Ser Cys Arg Ile Leu Thr Ser Asp Val Phe
 1055 1060 1065
 Gln Asp Cys Asn Lys Leu Val Asp Pro Glu Pro Tyr Leu Asp Val
 1070 1075 1080
 Cys Ile Tyr Asp Thr Cys Ser Cys Glu Ser Ile Gly Asp Cys Ala
 1085 1090 1095
 Cys Phe Cys Asp Thr Ile Ala Ala Tyr Ala His Val Cys Ala Gln
 1100 1105 1110
 His Gly Lys Val Val Thr Trp Arg Thr Ala Thr Leu Cys Pro Gln
 1115 1120 1125
 Ser Cys Glu Glu Arg Asn Leu Arg Glu Asn Gly Tyr Glu Cys Glu
 1130 1135 1140
 Trp Arg Tyr Asn Ser Cys Ala Pro Ala Cys Gln Val Thr Cys Gln
 1145 1150 1155
 His Pro Glu Pro Leu Ala Cys Pro Val Gln Cys Val Glu Gly Cys
 1160 1165 1170
 His Ala His Cys Pro Pro Gly Lys Ile Leu Asp Glu Leu Leu Gln
 1175 1180 1185
 Thr Cys Val Asp Pro Glu Asp Cys Pro Val Cys Glu Val Ala Gly
 1190 1195 1200
 Arg Arg Phe Ala Ser Gly Lys Lys Val Thr Leu Asn Pro Ser Asp
 1205 1210 1215
 Pro Glu His Cys Gln Ile Cys His Cys Asp Val Val Asn Leu Thr
 1220 1225 1230
 Cys Glu Ala Cys Gln Glu Pro Gly Gly Leu Val Val Pro Pro Thr
 1235 1240 1245
 Asp Ala Pro Val Ser Pro Thr Thr Leu Tyr Val Glu Asp Ile Ser
 1250 1255 1260
 Glu Pro Pro Leu His Asp Phe Tyr Cys Ser Arg Leu Leu Asp Leu
 1265 1270 1275
 Val Phe Leu Leu Asp Gly Ser Ser Arg Leu Ser Glu Ala Glu Phe
 1280 1285 1290
 Glu Val Leu Lys Ala Phe Val Val Asp Met Met Glu Arg Leu Arg
 1295 1300 1305
 Ile Ser Gln Lys Trp Val Arg Val Ala Val Val Glu Tyr His Asp

1310	1315	1320
Gly Ser His Ala Tyr Ile Gly Leu Lys Asp Arg Lys Arg Pro Ser		
1325	1330	1335
Glu Leu Arg Arg Ile Ala Ser Gln Val Lys Tyr Ala Gly Ser Gln		
1340	1345	1350
Val Ala Ser Thr Ser Glu Val Leu Lys Tyr Thr Leu Phe Gln Ile		
1355	1360	1365
Phe Ser Lys Ile Asp Arg Pro Glu Ala Ser Arg Ile Ala Leu Leu		
1370	1375	1380
Leu Met Ala Ser Gln Glu Pro Gln Arg Met Ser Arg Asn Phe Val		
1385	1390	1395
Arg Tyr Val Gln Gly Leu Lys Lys Lys Lys Val Ile Val Ile Pro		
1400	1405	1410
Val Gly Ile Gly Pro His Ala Asn Leu Lys Gln Ile Arg Leu Ile		
1415	1420	1425
Glu Lys Gln Ala Pro Glu Asn Lys Ala Phe Val Leu Ser Ser Val		
1430	1435	1440
Asp Glu Leu Glu Gln Gln Arg Asp Glu Ile Val Ser Tyr Leu Cys		
1445	1450	1455
Asp Leu Ala Pro Glu Ala Pro Pro Pro Thr Leu Pro Pro His Met		
1460	1465	1470
Ala Gln Val Thr Val Gly Pro Gly Leu Leu Gly Val Ser Thr Leu		
1475	1480	1485
Gly Pro Lys Arg Asn Ser Met Val Leu Asp Val Ala Phe Val Leu		
1490	1495	1500
Glu Gly Ser Asp Lys Ile Gly Glu Ala Asp Phe Asn Arg Ser Lys		
1505	1510	1515
Glu Phe Met Glu Glu Val Ile Gln Arg Met Asp Val Gly Gln Asp		
1520	1525	1530
Ser Ile His Val Thr Val Leu Gln Tyr Ser Tyr Met Val Thr Val		
1535	1540	1545
Glu Tyr Pro Phe Ser Glu Ala Gln Ser Lys Gly Asp Ile Leu Gln		
1550	1555	1560
Arg Val Arg Glu Ile Arg Tyr Gln Gly Gly Asn Arg Thr Asn Thr		
1565	1570	1575
Gly Leu Ala Leu Arg Tyr Leu Ser Asp His Ser Phe Leu Val Ser		
1580	1585	1590
Gln Gly Asp Arg Glu Gln Ala Pro Asn Leu Val Tyr Met Val Thr		
1595	1600	1605

Gly Asn Pro Ala Ser Asp Glu Ile Lys Arg Leu Pro Gly Asp Ile
 1610 1615 1620
 Gln Val Val Pro Ile Gly Val Gly Pro Asn Ala Asn Val Gln Glu
 1625 1630 1635
 Leu Glu Arg Ile Gly Trp Pro Asn Ala Pro Ile Leu Ile Gln Asp
 1640 1645 1650
 Phe Glu Thr Leu Pro Arg Glu Ala Pro Asp Leu Val Leu Gln Arg
 1655 1660 1665
 Cys Cys Ser Gly Glu Gly Leu Gln Ile Pro Thr Leu Ser Pro Ala
 1670 1675 1680
 Pro Gly Pro Arg Leu Thr Gln Val Ser Val Leu Gln Tyr Gly Ser
 1685 1690 1695
 Ile Thr Thr Ile Asp Val Pro Trp Asn Val Val Pro Glu Lys Ala
 1700 1705 1710
 His Leu Leu Ser Leu Val Asp Val Met Gln Arg Glu Gly Gly Pro
 1715 1720 1725
 Ser Gln Ile Gly Asp Ala Leu Gly Phe Ala Val Arg Tyr Leu Thr
 1730 1735 1740
 Ser Glu Met His Gly Ala Arg Pro Gly Ala Ser Lys Ala Val Val
 1745 1750 1755
 Ile Leu Val Thr Asp Val Ser Val Asp Ser Val Asp Ala Ala Ala
 1760 1765 1770
 Asp Ala Ala Arg Ser Asn Arg Val Thr Val Phe Pro Ile Gly Ile
 1775 1780 1785
 Gly Asp Arg Tyr Asp Ala Ala Gln Leu Arg Ile Leu Ala Gly Pro
 1790 1795 1800
 Ala Gly Asp Ser Asn Val Val Lys Leu Gln Arg Ile Glu Asp Leu
 1805 1810 1815
 Pro Thr Met Val Thr Leu Gly Asn Ser Phe Leu His Lys Leu Cys
 1820 1825 1830
 Ser Gly Phe Val Arg Ile Cys Met Asp Glu Asp Gly Asn Glu Lys
 1835 1840 1845
 Arg Pro Gly Asp Val Trp Thr Leu Pro Asp Gln Cys His Thr Val
 1850 1855 1860
 Thr Cys Gln Pro Asp Gly Gln Thr Leu Leu Lys Ser His Arg Val
 1865 1870 1875
 Asn Cys Asp Arg Gly Leu Arg Pro Ser Cys Pro Asn Ser Gln Ser
 1880 1885 1890

Pro Val Lys Val Glu Glu Thr Cys Gly Cys Arg Trp Thr Cys Pro
1895 1900 1905

Cys Val Cys Thr Gly Ser Ser Thr Arg His Ile Val Thr Phe Asp
1910 1915 1920

Gly Gln Asn Phe Lys Leu Thr Gly Ser Cys Ser Tyr Val Leu Phe
1925 1930 1935

Gln Asn Lys Glu Gln Asp Leu Glu Val Ile Leu His Asn Gly Ala
1940 1945 1950

Cys Ser Pro Gly Ala Arg Gln Gly Cys Met Lys Ser Ile Glu Val
1955 1960 1965

Lys His Ser Ala Leu Ser Val Glu Leu His Ser Asp Met Glu Val
1970 1975 1980

Thr Val Asn Gly Arg Leu Val Ser Val Pro Tyr Val Gly Gly Asn
1985 1990 1995

Met Glu Val Asn Val Tyr Gly Ala Ile Met His Glu Val Arg Phe
2000 2005 2010

Asn His Leu Gly His Ile Phe Thr Phe Thr Pro Gln Asn Asn Glu
2015 2020 2025

Phe Gln Leu Gln Leu Ser Pro Lys Thr Phe Ala Ser Lys Thr Tyr
2030 2035 2040

Gly Leu Cys Gly Ile Cys Asp Glu Asn Gly Ala Asn Asp Phe Met
2045 2050 2055

Leu Arg Asp Gly Thr Val Thr Thr Asp Trp Lys Thr Leu Val Gln
2060 2065 2070

Glu Trp Thr Val Gln Arg Pro Gly Gln Thr Cys Gln Pro Ile Leu
2075 2080 2085

Glu Glu Gln Cys Leu Val Pro Asp Ser Ser His Cys Gln Val Leu
2090 2095 2100

Leu Leu Pro Leu Phe Ala Glu Cys His Lys Val Leu Ala Pro Ala
2105 2110 2115

Thr Phe Tyr Ala Ile Cys Gln Gln Asp Ser Cys His Gln Glu Gln
2120 2125 2130

Val Cys Glu Val Ile Ala Ser Tyr Ala His Leu Cys Arg Thr Asn
2135 2140 2145

Gly Val Cys Val Asp Trp Arg Thr Pro Asp Phe Cys Ala Met Ser
2150 2155 2160

Cys Pro Pro Ser Leu Val Tyr Asn His Cys Glu His Gly Cys Pro
2165 2170 2175

Arg His Cys Asp Gly Asn Val Ser Ser Cys Gly Asp His Pro Ser
2180 2185 2190

Glu Gly Cys Phe Cys Pro Pro Asp Lys Val Met Leu Glu Gly Ser
2195 2200 2205

Cys Val Pro Glu Glu Ala Cys Thr Gln Cys Ile Gly Glu Asp Gly
2210 2215 2220

Val Gln His Gln Phe Leu Glu Ala Trp Val Pro Asp His Gln Pro
2225 2230 2235

Cys Gln Ile Cys Thr Cys Leu Ser Gly Arg Lys Val Asn Cys Thr
2240 2245 2250

Thr Gln Pro Cys Pro Thr Ala Lys Ala Pro Thr Cys Gly Leu Cys
2255 2260 2265

Glu Val Ala Arg Leu Arg Gln Asn Ala Asp Gln Cys Cys Pro Glu
2270 2275 2280

Tyr Glu Cys Val Cys Asp Pro Val Ser Cys Asp Leu Pro Pro Val
2285 2290 2295

Pro His Cys Glu Arg Gly Leu Gln Pro Thr Leu Thr Asn Pro Gly
2300 2305 2310

Glu Cys Arg Pro Asn Phe Thr Cys Ala Cys Arg Lys Glu Glu Cys
2315 2320 2325

Lys Arg Val Ser Pro Pro Ser Cys Pro Pro His Arg Leu Pro Thr
2330 2335 2340

Leu Arg Lys Thr Gln Cys Cys Asp Glu Tyr Glu Cys Ala Cys Asn
2345 2350 2355

Cys Val Asn Ser Thr Val Ser Cys Pro Leu Gly Tyr Leu Ala Ser
2360 2365 2370

Thr Ala Thr Asn Asp Cys Gly Cys Thr Thr Thr Thr Cys Leu Pro
2375 2380 2385

Asp Lys Val Cys Val His Arg Ser Thr Ile Tyr Pro Val Gly Gln
2390 2395 2400

Phe Trp Glu Glu Gly Cys Asp Val Cys Thr Cys Thr Asp Met Glu
2405 2410 2415

Asp Ala Val Met Gly Leu Arg Val Ala Gln Cys Ser Gln Lys Pro
2420 2425 2430

Cys Glu Asp Ser Cys Arg Ser Gly Phe Thr Tyr Val Leu His Glu
2435 2440 2445

Gly Glu Cys Cys Gly Arg Cys Leu Pro Ser Ala Cys Glu Val Val
2450 2455 2460

Thr Gly Ser Pro Arg Gly Asp Ser Gln Ser Ser Trp Lys Ser Val

2465 2470 2475
Gly Ser Gln Trp Ala Ser Pro Glu Asn Pro Cys Leu Ile Asn Glu
2480 2485 2490
Cys Val Arg Val Lys Glu Glu Val Phe Ile Gln Gln Arg Asn Val
2495 2500 2505
Ser Cys Pro Gln Leu Glu Val Pro Val Cys Pro Ser Gly Phe Gln
2510 2515 2520
Leu Ser Cys Lys Thr Ser Ala Cys Cys Pro Ser Cys Arg Cys Glu
2525 2530 2535
Arg Met Glu Ala Cys Met Leu Asn Gly Thr Val Ile Gly Pro Gly
2540 2545 2550
Lys Thr Val Met Ile Asp Val Cys Thr Thr Cys Arg Cys Met Val
2555 2560 2565
Gln Val Gly Val Ile Ser Gly Phe Lys Leu Glu Cys Arg Lys Thr
2570 2575 2580
Thr Cys Asn Pro Cys Pro Leu Gly Tyr Lys Glu Glu Asn Asn Thr
2585 2590 2595
Gly Glu Cys Cys Gly Arg Cys Leu Pro Thr Ala Cys Thr Ile Gln
2600 2605 2610
Leu Arg Gly Gly Gln Ile Met Thr Leu Lys Arg Asp Glu Thr Leu
2615 2620 2625
Gln Asp Gly Cys Asp Thr His Phe Cys Lys Val Asn Glu Arg Gly
2630 2635 2640
Glu Tyr Phe Trp Glu Lys Arg Val Thr Gly Cys Pro Pro Phe Asp
2645 2650 2655
Glu His Lys Cys Leu Ala Glu Gly Gly Lys Ile Met Lys Ile Pro
2660 2665 2670
Gly Thr Cys Cys Asp Thr Cys Glu Glu Pro Glu Cys Asn Asp Ile
2675 2680 2685
Thr Ala Arg Leu Gln Tyr Val Lys Val Gly Ser Cys Lys Ser Glu
2690 2695 2700
Val Glu Val Asp Ile His Tyr Cys Gln Gly Lys Cys Ala Ser Lys
2705 2710 2715
Ala Met Tyr Ser Ile Asp Ile Asn Asp Val Gln Asp Gln Cys Ser
2720 2725 2730
Cys Cys Ser Pro Thr Arg Thr Glu Pro Met Gln Val Ala Leu His
2735 2740 2745
Cys Thr Asn Gly Ser Val Val Tyr His Glu Val Leu Asn Ala Met
2750 2755 2760

Glu Cys Lys Cys Ser Pro Arg Lys Cys Ser Lys
2765 2770

<210> 198

<211> 559

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 198

Met Glu Pro Gln Val Thr Leu Asn Val Thr Phe Lys Asn Glu Ile Gln
1 5 10 15

Ser Phe Leu Val Ser Asp Pro Glu Asn Thr Thr Trp Ala Asp Ile Glu
20 25 30

Ala Met Val Lys Val Ser Phe Asp Leu Asn Thr Ile Gln Ile Lys Tyr
35 40 45

Leu Asp Glu Glu Asn Glu Glu Val Ser Ile Asn Ser Gln Gly Glu Tyr
50 55 60

Glu Glu Ala Leu Lys Met Ala Val Lys Gln Gly Asn Gln Leu Gln Met
65 70 75 80

Gln Val His Glu Gly His His Val Val Asp Glu Ala Pro Pro Pro Val
85 90 95

Val Gly Ala Lys Arg Leu Ala Ala Arg Ala Gly Lys Lys Pro Leu Ala
100 105 110

His Tyr Ser Ser Leu Val Arg Val Leu Gly Ser Asp Met Lys Thr Pro
115 120 125

Glu Asp Pro Ala Val Gln Ser Phe Pro Leu Val Pro Cys Asp Thr Asp
130 135 140

Gln Pro Gln Asp Lys Pro Pro Asp Trp Phe Thr Ser Tyr Leu Glu Thr
145 150 155 160

Phe Arg Glu Gln Val Val Asn Glu Thr Val Glu Lys Leu Glu Gln Lys
165 170 175

Leu His Glu Lys Leu Val Leu Gln Asn Pro Ser Leu Gly Ser Cys Pro
180 185 190

Ser Glu Val Ser Met Pro Thr Ser Glu Glu Thr Leu Phe Leu Pro Glu
195 200 205

Asn Gln Phe Ser Trp His Ile Ala Cys Asn Asn Cys Gln Arg Arg Ile
210 215 220

Val Gly Val Arg Tyr Gln Cys Ser Leu Cys Pro Ser Tyr Asn Ile Cys
225 230 235 240

Glu Asp Cys Glu Ala Gly Pro Tyr Gly His Asp Thr Asn His Val Leu

245 250 255
 Leu Lys Leu Arg Arg Pro Val Val Gly Ser Ser Glu Pro Phe Cys His
 260 265 270
 Ser Lys Tyr Ser Thr Pro Arg Leu Pro Ala Ala Leu Glu Gln Val Arg
 275 280 285
 Leu Gln Lys Gln Val Asp Lys Asn Phe Leu Lys Ala Glu Lys Gln Arg
 290 295 300
 Leu Arg Ala Glu Lys Lys Gln Arg Lys Ala Glu Val Lys Glu Leu Lys
 305 310 315 320
 Lys Gln Leu Lys Leu His Arg Lys Ile His Leu Trp Asn Ser Ile His
 325 330 335
 Gly Leu Gln Ser Pro Lys Ser Pro Leu Gly Arg Pro Glu Ser Leu Leu
 340 345 350
 Gln Ser Asn Thr Leu Met Leu Pro Leu Gln Pro Cys Thr Ser Val Met
 355 360 365
 Pro Met Leu Ser Ala Ala Phe Val Asp Glu Asn Leu Pro Asp Gly Thr
 370 375 380
 His Leu Gln Pro Gly Thr Lys Phe Ile Lys His Trp Arg Met Lys Asn
 385 390 395 400
 Thr Gly Asn Val Lys Trp Ser Ala Asp Thr Lys Leu Lys Phe Met Trp
 405 410 415
 Gly Asn Leu Thr Leu Ala Ser Thr Glu Lys Lys Asp Val Leu Val Pro
 420 425 430
 Cys Leu Lys Ala Gly His Val Gly Val Val Ser Val Glu Phe Ile Ala
 435 440 445
 Pro Ala Leu Glu Gly Thr Tyr Thr Ser His Trp Arg Leu Ser His Lys
 450 455 460
 Gly Gln Gln Phe Gly Pro Arg Val Trp Cys Ser Ile Ile Val Asp Pro
 465 470 475 480
 Phe Pro Ser Glu Glu Ser Pro Asp Asn Ile Glu Lys Gly Met Ile Ser
 485 490 495
 Ser Ser Lys Thr Asp Asp Leu Thr Cys Gln Gln Glu Glu Thr Phe Leu
 500 505 510
 Leu Ala Lys Glu Glu Arg Gln Leu Gly Glu Val Thr Glu Gln Thr Glu
 515 520 525
 Gly Thr Ala Ala Cys Ile Pro Gln Lys Ala Lys Asn Val Ala Ser Glu
 530 535 540
 Arg Glu Leu Tyr Ile Pro Ser Val Asp Leu Leu Thr Ala Gln Met
 545 550 555

<210> 199
 <211> 929
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> A novel predicted alternative spliced variant protein product

 <400> 199

 Met Glu Pro Gln Val Thr Leu Asn Val Thr Phe Lys Asn Glu Ile Gln
 1 5 10 15

 Ser Phe Leu Val Ser Asp Pro Glu Asn Thr Thr Trp Ala Asp Ile Glu
 20 25 30

 Ala Met Val Lys Val Ser Phe Asp Leu Asn Thr Ile Gln Ile Lys Tyr
 35 40 45

 Leu Asp Glu Glu Asn Glu Glu Val Ser Ile Asn Ser Gln Gly Glu Tyr
 50 55 60

 Glu Glu Ala Leu Lys Met Ala Val Lys Gln Gly Asn Gln Leu Gln Met
 65 70 75 80

 Gln Val His Glu Gly His His Val Val Asp Glu Ala Pro Pro Pro Val
 85 90 95

 Val Gly Ala Lys Arg Leu Ala Ala Arg Ala Gly Lys Lys Pro Leu Ala
 100 105 110

 His Tyr Ser Ser Leu Val Arg Val Leu Gly Ser Asp Met Lys Thr Pro
 115 120 125

 Glu Asp Pro Ala Val Gln Ser Phe Pro Leu Val Pro Cys Asp Thr Asp
 130 135 140

 Gln Pro Gln Asp Lys Pro Pro Asp Trp Phe Thr Ser Tyr Leu Glu Thr
 145 150 155 160

 Phe Arg Glu Gln Val Val Asn Glu Thr Val Glu Lys Leu Glu Gln Lys
 165 170 175

 Leu His Glu Lys Leu Val Leu Gln Asn Pro Ser Leu Gly Ser Cys Pro
 180 185 190

 Ser Glu Val Ser Met Pro Thr Ser Glu Glu Thr Leu Phe Leu Pro Glu
 195 200 205

 Asn Gln Phe Ser Trp His Ile Ala Cys Asn Asn Cys Gln Arg Arg Ile
 210 215 220

 Val Gly Val Arg Tyr Gln Cys Ser Leu Cys Pro Ser Tyr Asn Ile Cys
 225 230 235 240

 Glu Asp Cys Glu Ala Gly Pro Tyr Gly His Asp Thr Asn His Val Leu
 245 250 255

 Leu Lys Leu Arg Arg Pro Val Val Gly Ser Ser Glu Pro Phe Cys His

260 265 270
 Ser Lys Tyr Ser Thr Pro Arg Leu Pro Ala Ala Leu Glu Gln Val Arg
 275 280 285
 Leu Gln Lys Gln Val Asp Lys Asn Phe Leu Lys Ala Glu Lys Gln Arg
 290 295 300
 Leu Arg Ala Glu Lys Lys Gln Arg Lys Ala Glu Val Lys Glu Leu Lys
 305 310 315 320
 Lys Gln Leu Lys Leu His Arg Lys Ile His Leu Trp Asn Ser Ile His
 325 330 335
 Gly Leu Gln Ser Pro Lys Ser Pro Leu Gly Arg Pro Glu Ser Leu Leu
 340 345 350
 Gln Ser Asn Thr Leu Met Leu Pro Leu Gln Pro Cys Thr Ser Val Met
 355 360 365
 Pro Met Leu Ser Ala Ala Phe Val Asp Glu Asn Leu Pro Asp Gly Thr
 370 375 380
 His Leu Gln Pro Gly Thr Lys Phe Ile Lys His Trp Arg Met Lys Asn
 385 390 395 400
 Thr Gly Asn Val Lys Trp Ser Ala Asp Thr Lys Leu Lys Phe Met Trp
 405 410 415
 Gly Asn Leu Thr Leu Ala Ser Thr Glu Lys Lys Asp Val Leu Val Pro
 420 425 430
 Cys Leu Lys Ala Gly His Val Gly Val Val Ser Val Glu Phe Ile Ala
 435 440 445
 Pro Ala Leu Glu Gly Thr Tyr Thr Ser His Trp Arg Leu Ser His Lys
 450 455 460
 Gly Gln Gln Phe Gly Pro Arg Val Trp Cys Ser Ile Ile Val Asp Pro
 465 470 475 480
 Phe Pro Ser Glu Glu Ser Pro Asp Asn Ile Glu Lys Gly Met Ile Ser
 485 490 495
 Ser Ser Lys Thr Asp Asp Leu Thr Cys Gln Gln Glu Glu Thr Phe Leu
 500 505 510
 Leu Ala Lys Glu Glu Arg Gln Leu Gly Glu Val Thr Glu Gln Thr Glu
 515 520 525
 Gly Thr Ala Ala Cys Ile Pro Gln Lys Ala Lys Asn Val Ala Ser Glu
 530 535 540
 Arg Glu Leu Tyr Ile Pro Ser Val Asp Leu Leu Thr Ala Gln Asp Leu
 545 550 555 560
 Leu Ser Phe Glu Leu Leu Asp Ile Asn Ile Val Gln Glu Leu Glu Arg
 565 570 575

Val Pro His Asn Thr Pro Val Asp Ser Met Val Ser Val Lys Arg Lys
580 585 590

Ala Glu Asn Ile Ala Ser Val Glu Glu Ala Glu Glu Asp Leu Ser Gly
595 600 605

Thr Gln Phe Val Cys Glu Thr Val Ile Arg Ser Leu Thr Leu Asp Ala
610 615 620

Ala Pro Asp His Asn Pro Pro Cys Arg Gln Lys Ser Leu Gln Met Thr
625 630 635 640

Phe Ala Leu Pro Glu Gly Pro Leu Gly Asn Glu Lys Glu Glu Ile Ile
645 650 655

His Ile Ala Glu Glu Glu Ala Val Met Glu Glu Glu Glu Asp Glu Glu
660 665 670

Asp Glu Glu Glu Glu Asp Glu Leu Lys Asp Glu Val Gln Ser Gln Ser
675 680 685

Ser Ala Ser Ser Glu Asp Tyr Ile Ile Ile Leu Pro Glu Cys Phe Asp
690 695 700

Thr Ser Arg Pro Leu Gly Asp Ser Met Tyr Ser Ser Ala Leu Ser Gln
705 710 715 720

Pro Gly Leu Glu Arg Gly Ala Glu Gly Lys Pro Gly Val Glu Ala Gly
725 730 735

Gln Glu Pro Ala Glu Ala Gly Glu Arg Leu Pro Gly Gly Glu Asn Gln
740 745 750

Pro Gln Glu His Ser Ile Ser Asp Ile Leu Thr Thr Ser Gln Thr Leu
755 760 765

Glu Thr Val Pro Leu Ile Pro Glu Val Val Glu Leu Pro Pro Ser Leu
770 775 780

Pro Arg Ser Ser Pro Cys Val His His His Gly Ser Pro Gly Val Asp
785 790 795 800

Leu Pro Val Thr Ile Pro Glu Val Ser Ser Val Pro Asp Gln Ile Arg
805 810 815

Gly Glu Pro Arg Gly Ser Ser Gly Leu Val Asn Ser Arg Gln Lys Ser
820 825 830

Tyr Asp His Ser Arg His His His Gly Ser Ser Ile Ala Gly Gly Leu
835 840 845

Val Lys Gly Ala Leu Ser Val Ala Ala Ser Ala Tyr Lys Ala Leu Phe
850 855 860

Ala Gly Pro Pro Val Thr Ala Gln Pro Ile Ile Ser Glu Asp Gln Thr
865 870 875 880

Ala Ala Leu Met Ala Arg Leu Phe Glu Met Gly Phe Cys Asp Arg Gln
885 890 895

Leu Asn Leu Arg Leu Leu Lys Lys His Asn Tyr Asn Ile Leu Gln Val
900 905 910

Val Thr Glu Leu Leu Gln Leu Asn Asn Asn Asp Trp Tyr Ser Gln Arg
915 920 925

Tyr

<210> 200
<211> 875
<212> PRT
<213> Artificial sequence

<220>
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<400> 200

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1 5 10 15

Ser Phe Leu Val Ser Asp Pro Glu Asn Thr Thr Trp Ala Asp Ile Glu
20 25 30

Ala Met Val Lys Val Ser Phe Asp Leu Asn Thr Ile Gln Ile Lys Tyr
35 40 45

Leu Asp Glu Glu Asn Glu Glu Val Ser Ile Asn Ser Gln Gly Glu Tyr
50 55 60

Glu Glu Ala Leu Lys Met Ala Val Lys Gln Gly Asn Gln Leu Gln Met
65 70 75 80

Gln Val His Glu Gly His His Val Val Asp Glu Ala Pro Pro Pro Val
85 90 95

Val Gly Ala Lys Arg Leu Ala Ala Arg Ala Gly Lys Lys Pro Leu Ala
100 105 110

His Tyr Ser Ser Leu Val Arg Val Leu Gly Ser Asp Met Lys Thr Pro
115 120 125

Glu Asp Pro Ala Val Gln Ser Phe Pro Leu Val Pro Cys Asp Thr Asp
130 135 140

Gln Pro Gln Asp Lys Pro Pro Asp Trp Phe Thr Ser Tyr Leu Glu Thr
145 150 155 160

Phe Arg Glu Gln Val Val Asn Glu Thr Val Glu Lys Leu Glu Gln Lys
165 170 175

Leu His Glu Lys Leu Val Leu Gln Asn Pro Ser Leu Gly Ser Cys Pro
180 185 190

Ser Glu Val Ser Met Pro Thr Ser Glu Glu Thr Leu Phe Leu Pro Glu
195 200 205

Asn Gln Phe Ser Trp His Ile Ala Cys Asn Asn Cys Gln Arg Arg Ile
210 215 220

Val Gly Val Arg Tyr Gln Cys Ser Leu Cys Pro Ser Tyr Asn Ile Cys
225 230 235 240

Glu Asp Cys Glu Ala Gly Pro Tyr Gly His Asp Thr Asn His Val Leu
245 250 255

Leu Lys Leu Arg Arg Pro Val Val Gly Ser Ser Glu Pro Phe Cys His
260 265 270

Ser Lys Tyr Ser Thr Pro Arg Leu Pro Ala Ala Leu Glu Gln Val Arg
275 280 285

Leu Gln Lys Gln Val Asp Lys Asn Phe Leu Lys Ala Glu Lys Gln Arg
290 295 300

Leu Arg Ala Glu Lys Lys Gln Arg Lys Ala Glu Val Lys Glu Leu Lys
305 310 315 320

Lys Gln Leu Lys Leu His Arg Lys Ile His Leu Trp Asn Ser Ile His
325 330 335

Gly Leu Gln Ser Pro Lys Ser Pro Leu Gly Arg Pro Glu Ser Leu Leu
340 345 350

Gln Ser Asn Thr Leu Met Leu Pro Leu Gln Pro Cys Thr Ser Val Met
355 360 365

Pro Met Leu Ser Ala Ala Phe Val Asp Glu Asn Leu Pro Asp Gly Thr
370 375 380

His Leu Gln Pro Gly Thr Lys Phe Ile Lys His Trp Arg Met Lys Asn
385 390 395 400

Thr Gly Asn Val Lys Trp Ser Ala Asp Thr Lys Leu Lys Phe Met Trp
405 410 415

Gly Asn Leu Thr Leu Ala Ser Thr Glu Lys Lys Asp Val Leu Val Pro
420 425 430

Cys Leu Lys Ala Gly His Val Gly Val Val Ser Val Glu Phe Ile Ala
435 440 445

Pro Ala Leu Glu Gly Thr Tyr Thr Ser His Trp Arg Leu Ser His Lys
450 455 460

Gly Gln Gln Phe Gly Pro Arg Val Trp Cys Ser Ile Ile Val Asp Pro
465 470 475 480

Phe Pro Ser Glu Glu Ser Pro Asp Asn Ile Glu Lys Gly Met Ile Ser
485 490 495

Ser Ser Lys Thr Asp Asp Leu Thr Cys Gln Gln Glu Glu Thr Phe Leu
500 505 510

Leu Ala Lys Glu Glu Arg Gln Leu Gly Glu Val Thr Glu Gln Thr Glu
515 520 525

Gly Thr Ala Ala Cys Ile Pro Gln Lys Ala Lys Asn Val Ala Ser Glu
530 535 540

Arg Glu Leu Tyr Ile Pro Ser Val Asp Leu Leu Thr Ala Gln Asp Leu
545 550 555 560

Leu Ser Phe Glu Leu Leu Asp Ile Asn Ile Val Gln Glu Leu Glu Arg
565 570 575

Val Pro His Asn Thr Pro Val Asp Val Thr Pro Cys Met Ser Pro Leu
580 585 590

Pro His Asp Ser Pro Leu Ile Glu Lys Pro Gly Leu Gly Gln Ile Glu
595 600 605

Glu Glu Asn Glu Gly Ala Gly Phe Lys Ala Leu Pro Asp Ser Met Val
610 615 620

Ser Val Lys Arg Lys Ala Glu Asn Ile Ala Ser Val Glu Glu Ala Glu
625 630 635 640

Glu Asp Leu Ser Gly Thr Gln Phe Val Cys Glu Thr Val Ile Arg Ser
645 650 655

Leu Thr Leu Asp Ala Ala Pro Asp His Asn Pro Pro Cys Arg Gln Lys
660 665 670

Ser Leu Gln Met Thr Phe Ala Leu Pro Glu Gly Pro Leu Gly Asn Glu
675 680 685

Lys Glu Glu Ile Ile His Ile Ala Glu Glu Glu Ala Val Met Glu Glu
690 695 700

Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Leu Lys Asp Glu
705 710 715 720

Val Gln Ser Gln Ser Ser Ala Ser Ser Glu Asp Tyr Ile Ile Ile Leu
725 730 735

Pro Glu Cys Phe Asp Thr Ser Arg Pro Leu Gly Asp Ser Met Tyr Ser
740 745 750

Ser Ala Leu Ser Gln Pro Gly Leu Glu Arg Gly Ala Glu Gly Lys Pro
755 760 765

Gly Val Glu Ala Gly Gln Glu Pro Ala Glu Ala Gly Glu Arg Leu Pro
770 775 780

Gly Gly Glu Asn Gln Pro Gln Glu His Ser Ile Ser Asp Ile Leu Thr
785 790 795 800

Thr Ser Gln Thr Leu Glu Thr Val Pro Leu Ile Pro Glu Val Val Glu
805 810 815

Leu Pro Pro Ser Leu Pro Arg Ser Ser Pro Cys Val His His His Gly
820 825 830

Ser Pro Gly Val Asp Leu Pro Val Thr Ile Pro Glu Val Ser Ser Val
835 840 845

Pro Asp Gln Ile Arg Gly Glu Pro Arg Gly Ser Ser Gly Leu Val Asn
850 855 860

Ser Arg Gln Lys Ser Tyr Asp His Ser Ser Gln
865 870 875

<210> 201
<211> 89
<212> DNA
<213> Artificial sequence

<220>
<223> Ephrine receptor B1 novel alternative spliced exon

<400> 201
cctcatctca cctcaacccc cttgttgcaa agtaaggctg gtgcttctg tttctcagc 60
aattagcatg gaaaacagac ctcccaggc 89

<210> 202
<211> 106
<212> DNA
<213> Artificial sequence

<220>
<223> FSH receptor novel alternative spliced exon

<400> 202
aggaacagaa ggaccaggac tcctacagaa ccaaagtcc tattagccaa atatccatct 60
ggccaaggctg tgttgaggga accggagtct ctctctcat ccatgt 106

<210> 203
<211> 73
<212> DNA
<213> Artificial sequence

<220>
<223> HPA2 novel alternative spliced exon

<400> 203
agattctttt ttgtttcact tgtattcatt tctttgattc actcggaatc tgttttgatg 60
catggtgaaa ggt 73

<210> 204
<211> 98
<212> DNA
<213> Artificial sequence

<220>
<223> HPA2 novel alternative spliced exon

<400> 204
agttcctctt gctgaagag aatttgaacc actctttgtc tataaggagc tctctgcaac 60
acagtctaga acttgagaga aatctgaatg attttata 98

<210> 205
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 205

Gly Val Leu Gln Tyr Gly Cys Gln Trp Gly Arg Leu Asp Cys Asn Thr
1 5 10 15

Thr Ser

<210> 206
<211> 29
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 206

Trp Asn Ser Gln Arg Leu Arg Met Ser Trp Ser Arg Ser Ser Lys Ser
1 5 10 15

Ile Thr Trp Gly Met Tyr Leu Leu Leu Asn Leu Leu Gly
20 25

<210> 207
<211> 82
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 207

Asp Arg Gly Ser Ala Gly Arg Val Ser Gly Ala Phe Pro Leu Leu Pro
1 5 10 15

Gly Arg Gly Gln Arg Cys Pro His Val Cys Ile His His Gly Cys Arg
20 25 30

Pro Ser Leu Leu Leu Leu Pro His Val Leu Val Arg Ala Gln Cys Cys
35 40 45

Gln Pro Leu Arg Gly Cys Ala Gly Cys Val His Ala Ser Leu Pro Glu
50 55 60

Val Ser Gly Cys Pro Phe Pro Gly Leu His Leu Leu Pro Pro Ser Thr
65 70 75 80

Pro Cys

<210> 208
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 208

Ala His Leu Asp Arg Phe Cys Ser Trp Arg Arg Leu
1 5 10

<210> 209
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 209

Gly Cys Ala Cys Ser Leu Ser Leu Gly
1 5

<210> 210
<211> 28
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 210

Ser Phe Thr Arg Gln Gln Lys Ile Gly Gly Tyr Ser Val Ser Ile Ser
1 5 10 15

Ala Cys His Trp Pro Ser Leu His Phe Phe Ile His
20 25

<210> 211
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 211

Asn Tyr Ile Lys Trp Val Phe Gly Gly Pro Gly
1 5 10

<210> 212
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 212

Gly Gly Ser Glu Tyr His Gly
1 5

<210> 213
<211> 58
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 213

Leu Ala Lys Leu Asp Ile Thr Arg Leu Ser Pro Arg Met Pro Pro Val
1 5 10 15

Pro Ser Ala His Pro Thr Ala Thr Leu Ser Gly Lys Glu Pro Pro Arg

20 25 30
Ala Pro Val Thr Glu Ala Phe Ser Glu Leu Thr Thr Met Leu Pro Leu
35 40 45

Cys Pro Ala Pro Val His His Leu Leu Pro
50 55

<210> 214
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 214

Ile Val Ala Val Gly Gly Leu Leu Pro Cys Ala Leu Leu Pro Ile Gln
1 5 10 15

Ala

<210> 215
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 215

Ala Asn Lys Pro Ser Ser Gly Ser Lys His Ser
1 5 10

<210> 216
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 216

Gly Asn Gly Leu Ile Ala Lys Arg Leu Cys Thr Ala Ile Ser Ser Ser
1 5 10 15

Ile Thr Ala Gln Ala Glu Gly Ser Leu Glu Lys Cys Thr Arg Gly Val
20 25 30

<210> 217
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 217

Arg Leu Pro Pro Leu Gln Pro Gln Trp His Leu
1 5 10

<210> 218
<211> 78

<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 218

Val Leu Thr Thr Val Gln Ser Ala Leu Ile Leu Lys Met Ala Gln Thr
1 5 10 15

Val Trp Lys Asn Val Gln Met Ala Tyr Arg Gly Gln Thr Val Ser Phe
20 25 30

Ser Ser Met Leu Ile Gln Ile Gly Ser Ala Thr His Ala Ile Gln Thr
35 40 45

Ala Pro Lys Gly Val Thr Val Pro Leu Val Met Thr Ala Phe Thr His
50 55 60

Gly Arg Ala Ile Pro Leu Tyr His Asn Met Leu Glu Leu Pro
65 70 75

<210> 219
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 219

Arg Thr Phe His Thr
1 5

<210> 220
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 220

Trp Leu Pro Arg Arg Thr Trp Thr Ser Ala Ala Ser Thr Trp Arg Thr
1 5 10 15

Arg Arg Gly Leu Gly Thr Met
20

<210> 221
<211> 24
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 221

Arg Trp His Gln Gln Gly Val Trp Val His Arg Glu Gly Ser Gly Glu
1 5 10 15

Gln Leu His Gly Pro Asp Val Gly
20

<210> 222
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 222

Lys Thr Asn Pro Arg Val Cys Ile Gln Arg Thr Val Arg Arg Lys Leu
1 5 10 15

Val

<210> 223
<211> 34
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 223

Asn Arg Arg Thr Arg Thr Pro Thr Glu Pro Asn Val Leu Leu Ala Lys
1 5 10 15

Tyr Pro Ser Gly Gln Gly Val Leu Glu Glu Pro Glu Ser Leu Ser Ser
20 25 30

Ser Ile

<210> 224
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 224

Pro Gln Leu Arg Ser Trp Val His Tyr Thr Phe Tyr His Gln Leu Ala
1 5 10 15

Ser Ile Lys Lys Glu Asn Gln Ala Gly Trp Asp Ser Gln Arg Gln Ala
20 25 30

Gly Ser Pro Val Pro Ala Ala Ala Leu Trp Ala Gly Gly Pro Lys Val
35 40 45

Gln Val Ser Ala Thr Glu Trp Pro Ala Leu Ser Asp Gly Gly Arg Arg
50 55 60

Asp Pro Pro Arg Ile Glu Ala Pro Pro Pro Ser Gly Arg Pro Asp Ile
65 70 75 80

Gly His Pro Ser Ser His His Gly Leu Leu Cys Gly Gln Glu Cys Gln
85 90 95

Cys Phe Gly Leu Pro Leu Pro Ile Ser Tyr Pro His Thr His Gly Tyr
100 105 110

Gln Trp Ala Cys Trp Ala Ala Ser Thr Pro Pro Leu Gln
115 120 125

<210> 225

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 225

Gln Trp Leu Ile His Thr Leu Gln Glu Arg Arg Phe Gly Leu Lys Val
1 5 10 15

Trp

<210> 226

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 226

Met Val Glu His Phe Arg Ile Ala Gly Gln Ser Gly His
1 5 10

<210> 227

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 227

Thr Thr Gly Ser Leu Ser Ser Thr Ser Ala
1 5 10

<210> 228

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 228

Val Leu Ile Pro Ile Ala Gln Glu Lys Leu Ile Phe Gln
1 5 10

<210> 229

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 229

Ala Gly Gln Lys His Gly Gly Gln Val Leu Tyr Ser Lys Glu Ile Leu

1 5 10 15

Cys Leu

<210> 230
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 230

Glu Phe Leu Arg Ser Ile Leu Gly Asn Arg Lys Phe Pro Ser His
1 5 10 15

<210> 231
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 231

Ala Asn Val His Ser Gly Thr Cys Cys Arg Pro Cys Cys Tyr Ser Cys
1 5 10 15

Cys Leu Tyr Val Trp
20

<210> 232
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 232

Ala Ser Gln Lys Cys Gly Glu Ala
1 5

<210> 233
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 233

Leu Tyr Ser Gln Thr Ser Leu Pro Ser His Cys Ser Pro Trp Arg Ile
1 5 10 15

Ser Gln Val Leu
20

<210> 234
<211> 49
<212> PRT
<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 234

Phe Ser Lys Ser Ile Leu Glu Lys Lys Lys Leu Asn Trp His Ser Ser
1 5 10 15

Leu Thr Gln Leu Trp Lys Leu Thr Trp Arg Ile Ile Pro Ala Met Leu
20 25 30

Lys Thr Glu Met Asp Gly Asn Met Pro Val Phe Cys Cys Val Lys Arg
35 40 45

Ile

<210> 235

<211> 16

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 235

Leu Cys Arg Cys Val Tyr Trp Ser Thr Ser Leu His Gly Ser Trp Leu
1 5 10 15

<210> 236

<211> 55

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 236

Gly Leu Val Pro Ser Ile Leu Pro Ala Pro Gln Arg Ala Gln Arg Val
1 5 10 15

Pro Gln Arg Ala Glu Leu His Pro His Pro Gly Arg Pro Val Leu Arg
20 25 30

Pro Pro Leu His Trp Cys Gly Arg Val Ser Val Phe Gln Ser Pro Ala
35 40 45

Gly Glu Asp Lys Val His Leu
50 55

<210> 237

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 237

Gln Trp Arg Gly Thr Glu Asp Arg Leu Leu Val His Arg His Gly Ser
1 5 10 15

Arg

<210> 238
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 238

Val Ser Leu Leu Ala Val Val Pro Leu Ala Lys
1 5 10

<210> 239
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 239

Ser Val Ser Ala Glu Gln
1 5

<210> 240
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 240

Arg Thr Thr Arg Arg Thr Val Val Trp Phe Leu Pro Gln Lys Ser
1 5 10 15

<210> 241
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 241

Trp Asn Gly Ala Gln Gln Lys Gln Gly Val Cys Gly Ile
1 5 10

<210> 242
<211> 48
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 242

Tyr Val Ala Arg Glu Arg Glu Arg Val Ser Arg Ser Val Ile Val Ala
1 5 10 15

Cys Ile Asn Thr Val Thr Phe Val His Trp Leu Val Thr Val His Val
20 25 30

Cys Phe Ile Asn Glu Ala Ala Leu Asn Lys Phe Ile Phe Cys Leu Glu
35 40 45

<210> 243
<211> 10
<212> PRT
<213> Artificial sequence.

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 243

Ala Ala Ile Val Leu Met Ser Thr Trp Thr
1 5 10

<210> 244
<211> 13
<212> PRT
<213> Artificial sequence.

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 244

Asn Ala Leu Leu Leu Tyr Cys Gln Trp Met Cys Arg His
1 5 10

<210> 245
<211> 71
<212> PRT
<213> Artificial sequence.

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 245

Arg Ser Ser Lys Phe Asn Val Leu Glu Ile His Asn Gly Ser Cys Lys
1 5 10 15

Gln Pro Gln Pro Asn Leu Gln Gly Val Gln Lys Cys Phe Pro Gln Gly
20 25 30

Pro Leu Trp Tyr Asn Leu Arg Asn Ser Asn Leu Glu Thr Leu Cys Lys
35 40 45

Leu Cys Gln Trp Glu Tyr Gly Lys Cys Cys Gly Glu Ala Leu Cys Gly
50 55 60

Ser Ser Ile Cys Trp Arg Glu
65 70

<210> 246
<211> 46
<212> PRT
<213> Artificial sequence.

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 246

Pro Phe Met Val Gln Pro Gln Lys Gln Gln Leu Gly Asp Val Val Gln
1 5 10 15

Thr Met Ser Met Gly Ile Trp Lys Met Leu Trp Gly Gly Phe Met Trp
20 25 30

Lys Gln His Leu Leu Glu Arg Val Asn Met Trp Ser Arg Ile
35 40 45

<210> 247
<211> 31
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 247

Val Asp Lys Trp Ser Ser Cys Ser Gln Cys Ile Leu Leu Phe Arg Lys
1 5 10 15

Lys Ser Asp Ser Leu Pro Ser Arg His Ser Ala Ala Pro Leu Leu
20 25 30

<210> 248
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 248

Gly Arg Ser Pro Val Leu Ala Pro
1 5

<210> 249
<211> 169
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product
<400> 249

Gly Ala Arg Leu Ala Gly Trp Val Ser Gly Val Ser Trp Arg Thr Pro
1 5 10 15

Val Thr Gln Ala Pro Val Leu Ala Val Val Ser Ala Arg Val Gln Trp
20 25 30

Trp Leu Ala Pro Pro Asp Ser His Ala Gly Ala Pro Val Ala Ser Glu
35 40 45

Ala Leu Thr Ala Pro Cys Gln Ile Pro Ala Ser Ala Ala Leu Val Pro
50 55 60

Thr Val Pro Ala Ala Gln Trp Gly Pro Met Asp Ala Ser Ser Ala Pro
65 70 75 80

Ala His Leu Ala Thr Arg Ala Ala Ala Ala Glu Ala Thr Trp Met Ser
85 90 95

Ala Gly Trp Val Ser Pro Ala Ala Met Val Ala Pro Ala Ser Thr His
100 105 110

Leu Ala Pro Ser Ala Ala Ser Val Gln Leu Ala Thr Gln Gly His Tyr
115 120 125

Val Arg Thr Pro Arg Cys Pro Val His Pro His His Ala Val Thr Gly
130 135 140

Ala Pro Ala Gly Arg Val Ala Thr Ser Leu Thr Thr Val Pro Val Phe
145 150 155 160

Leu Gly Leu Arg Val Arg Ile Val Lys
165

<210> 250
<211> 41
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 250

Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn Arg His Leu
1 5 10 15

His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly Leu Leu Gln
20 25 30

Asn Gln Glu Thr Ala Glu Lys Ala Ala
35 40

<210> 251
<211> 41
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 251

Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn Arg His Leu
1 5 10 15

His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly Leu Leu Gln
20 25 30

Asn Gln Glu Thr Ala Glu Lys Ala Ala
35 40

<210> 252
<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 252

Arg Asn Ser Gly Lys Ser Cys Met Thr Val Phe Gly Arg Ala Phe Gly
1 5 10 15

Leu Asn Glu Thr Ile
20

<210> 253

<211> 21
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 253

Arg Asn Ser Gly Lys Ser Cys Met Thr Val Phe Gly Arg Ala Phe Gly
1 5 10 15

Leu Asn Glu Thr Ile
20

<210> 254
<211> 116
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 254

Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe
1 5 10 15

His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro
20 25 30

Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala Val Ser Pro Phe
35 40 45

Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg
50 55 60

Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser Phe His His
65 70 75 80

Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro Leu Arg Ile
85 90 95

Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln
100 105 110

Glu Pro Val Lys
115

<210> 255
<211> 41
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 255

Gly Gly Gly Ala Val Pro Glu Glu Ser Ala Asp His Asn Arg His Leu
1 5 10 15

His Arg Pro Pro Cys Gly Arg His His Val Cys Gly Gly Leu Leu Gln
20 25 30

Asn Gln Glu Thr Ala Glu Lys Ala Ala
35 40

<210> 256
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 256

Phe Val Phe Ala Leu Phe Lys Leu Gly Tyr Ser Leu Leu His Val Ser
1 5 10 15

Gln Leu Met Leu Ile Leu Thr
20

<210> 257
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 257

Trp Gln Gln Leu Gln Lys Arg Ile His Cys His Ser Gly Thr Ala Ser
1 5 10 15

Trp His Gln Gly
20

<210> 258
<211> 8
<212> PRT
<213> Artificial sequence

<220>
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<400> 258

Gly Gly Gly Arg Gly Lys Arg His
1 5

<210> 259
<211> 10
<212> PRT
<213> Artificial sequence

<220>
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<400> 259

Gly Asn Ala Ser Arg Leu His Thr Phe Thr
1 5 10

<210> 260
<211> 32
<212> PRT
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant protein product

<400> 260

Thr Glu Glu Val Leu Pro Gly Leu Arg Tyr Tyr Asp Glu Gln Leu Gln
1 5 10 15

Pro Pro Glu Gln Gln Ala Gln Glu Ser Ile His Lys Tyr Arg Cys Leu
20 25 30

<210> 261

<211> 43

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 261

Arg Ser Asn Met Ser Ser Phe Met Ile His Trp Leu Arg Pro Tyr Leu
1 5 10 15

Val Lys Lys Leu Arg Cys Trp Thr Val Ile Phe Met Pro Met Leu Met
20 25 30

His Ser Ser Phe Leu Asp Gln Gln Ala Lys Gln
35 40

<210> 262

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 262

Val Gly Cys Phe Cys Glu Val Leu Thr Cys Asn Asn Leu Val Met Ser
1 5 10 15

Cys

<210> 263

<211> 34

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 263

Ala Pro Gly Gln Val His Ser Pro Ala Asp Pro Pro Leu Trp His Pro
1 5 10 15

Leu His Arg Leu Arg Leu Leu Pro Arg Gly Arg Tyr Gly Asp Pro Ala
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Val Phe

<210> 264

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 264

Glu Met Cys Arg Ile Ile Ala Ala Tyr Val His Phe Thr Leu Ile Ser
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Arg Gly Ile

<210> 265

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 265

Leu Pro Val Ser Ser Ser Pro Leu Thr Thr Thr Trp
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<210> 266

<211> 75

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 266

Pro Ala Thr Leu Arg Thr Met Ala Gly Leu His Gly Pro Ser Gly Pro
1 5 10 15

Pro Val Leu Arg Ala Val Ala Met Glu Phe Ser Ser Ala Ala Ala Pro
20 25 30

Ala Ile Ala Ser Thr Thr Asp Val Arg Ala Pro Arg Ser Arg His Gly
35 40 45

Pro Ala Ile Phe Arg Ser Val Thr Arg Asp Leu Asn Arg Met Val Ala
50 55 60

Gly Ala Thr Gly Pro Arg Gly His Leu Val Leu
65 70 75

<210> 267

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 267

Val Ser Gly Ser Glu Gln Asp Leu Pro His Gln Leu His Val Glu
1 5 10 15

<210> 268

<211> 40

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 268

Val Lys Ile Gly Val Lys Lys Thr Trp Arg Met Glu Asp Val Asn Thr
1 5 10 15

Tyr Ala Cys Gln His His Arg Leu Met Ile Thr Leu Gln Asn Ile Pro
20 25 30

Val Pro Val Pro Val Gly Thr Met
35 40

<210> 269

<211> 36

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 269

Gly Glu Ser Lys Lys Lys Thr Trp Thr Leu Gln Val Met Gly Lys Asp
1 5 10 15

Ser Met Tyr Leu Val Arg Tyr Arg Ser Ser Lys Thr Asn Ser Asp Phe
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Pro Pro Arg Tyr
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<210> 270

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 270

Pro Tyr Lys Lys Ser Pro Leu Leu Ala
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<210> 271

<211> 75

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 271

Ala Gly Pro Arg Leu Cys Arg Glu Asp Leu Arg Pro Val Trp Glu Leu
1 5 10 15

Gln Trp Gln Pro Gly Arg Gly Leu Pro Tyr Pro Leu Trp Ala Gly Gly
20 25 30

Ala Pro Gly Gly Gly Leu Arg Glu Arg Leu Glu Ala Ala Arg Gly Leu
35 40 45

Pro Gly Pro Ala Glu Ala Ala Gln Arg Ser Leu Arg Pro Gln Pro Ala
50 55 60

His Glu Gly Ser Pro Arg Arg Arg Ala Arg Ser
65 70 75

<210> 272

<211> 65

<212> PRT

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant protein product

<400> 272

Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala Arg Glu
1 5 10 15

Ser Asn Ser Asp Arg Val Ser Ala Ser Lys Arg Arg Ser Ser Pro Ser
20 25 30

Lys Asp Gly Arg Ser Leu Cys Glu Arg His Val Leu Gly Val Phe Ser
35 40 45

Lys Val Arg Phe Cys Ser Gly Arg Lys Arg Pro Val Arg Arg Arg Pro
50 55 60

Ala
65

<210> 273

<211> 2502

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<220>

<221> misc feature

<222> (2145)..(2145)

<223> n is a, c, g, or t

<400> 273

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<210> 274

<211> 2496

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<220>

<221> misc. feature

<222> (2139) ..(2139)

<223> n is 'a', 'c', 'g', or 't'

<400> 274

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acaaatggtc gctgtattac gctgttctgg aaatgtgatg gggatgaaga ctgtgttgac 180

ggcagtgatg aaaagaactg tgtaagaag acgtgtgctg aatctgactt cgtgtgcaac 240
aatggccagt gtgttcccag ccgatggaag tgtgatggag atcctgactg cgaagatggt 300
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2496

<210> 275

<211> 2503

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<220>

<221> misc_feature

<222> (2146)..(2146)

<223> n is a, c, g, or t

<400> 275

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<210> 276

<211> 2480

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<220>

<221> misc feature

<222> (2123) .. (2123)

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<400> 276

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<221> misc feature

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<400> 277

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<223> n is a, c, g, or t

<400> 278

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<400> 279

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<211> 3903

<212> DNA

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<223> A novel predicted alternative spliced variant

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<212> DNA

<213> Artificial sequence

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<223> A novel predicted alternative spliced variant

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<211> 3971

<212> DNA

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<223> A novel predicted alternative spliced variant

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<213> Artificial sequence

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<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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<211> 2988

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<210> 293

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 293

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<210> 294

<211> 2013

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 294

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<211> 2200

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 295

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<210> 296

<211> 2189

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 296

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<210> 297

<211> 2028

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 297

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<211> 2025

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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<210> 299

<211> 2025

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 299

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<210> 300

<211> 2022

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 300

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<210> 301

<211> 2031

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 301
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<210> 302

<211> 2019

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 302
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<210> 303

<211> 2188

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 303

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<210> 304
<211> 567
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 304
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<210> 305
<211> 621
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 305
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gtgaatcaag attcaacata g 621

<210> 306
<211> 435
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 306
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<210> 307
<211> 627
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 307
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<210> 308
<211> 468
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 308
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ctgggtctga acaāagaagg agagatcatg aaaggcaacc atgtgaagaa gaacaagcct 300
gcagctcatt ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcaactgcac 360
gatctcacgg agttctccc atctggaagc gggaccccaa ccaagagcag aagtgtctct 420
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<210> 309
<211> 634
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

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aacaagttaa atgtcttttc ccgggtcaaa ctcttcgggt ccaagaagag gcgcagaaga 180
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ttcatcaatg atataccgtc agcagcagtc aggcggaggg tggatatctg gtctgaacaa 420
agaaggagag atcatgaaag gcaacctgtg gaagaagaac aagcctgcag ctcattttct 480
gcctaaacca ctgaaagtgg ccattgtaca ggagccatca ctgcacgac tcacggagtt 540
ctcccgatct ggaagcggga ccccaacca gagcagaagt gtctctggcg tgctgaacgg 600
aggcaaatcg atgagccaca atgaatcaac gtag 634

<210> 310
<211> 475
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 310
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gatgaggaca gcaattacag aacttttcac acctgagtg c aaattcaaag aatcagtgtt 180
tgaaaattat tatgtgacat attcatcaat gatataccgt cagcagcagt caggccgagg 240
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<210> 311
<211> 552
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 311
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gtgcagctga atgactacgt ggacatcac tgtccgcact atgaagatca ctctgtggca 180
gacgctgcca tggagcagta catactgtac ctgggtggagc atgaggagta ccagctgtgc 240
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ccggagaagc tgtctgagaa gttccagcgc ttcacacctt tcaccctggg caaggagttc 360
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gagaagagac ttgcagcaga tgaccagag gtgcgggttc tacatagcat cggtcacagt 480
gctgccccac gcctcttccc acttgctggg actgtgctgc tcttccact tctgtgctg 540

caaaccctgt ga

552

<210> 312
<211> 651
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

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ggcggggcag agcagtagt gctgtacatg gtgagccgca acggctaccg cacctgcaac 300
gccagccagg gcttcaagcg ctgggagtgc aaccggccgc acgccccgca cagcccatc 360
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ggccacgagt actactacat ctccacgcc actcacaacc tgcaactggaa gtgtctgagg 480
cagttcacca tgggcccga tgtgaagatc aacgtgctgg aagactttga gggagagaac 540
cctcaggtgc ccaagottga gaagagcatc agcgggacca gccccaaacg ggaacacctg 600
cccctggcgg tgggcacgcg cttcttctc atgacgttct tggcctccta g 651

<210> 313
<211> 639
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 313
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ggccacgagt actactacat ctccacgcc actcacaacc tgcaactggaa gtgtctgagg 480
atgaaggtgt tctgtctgct gcctccaaa gactttgagg gagagaacct tcaggtgccc 540
aagcttgaga agagcatcag cgggaccagc cccaaacggg aacacctgcc cctggccgtg 600
ggcagcgcct tcttctcat gacgttcttg gcctcctag 639

<210> 314
<211> 621
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 314

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cccagattcc agaggggtga ctacatatt gatgtctgta tcaatgacta cctggatgtt 180
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gcgatgcttt tgacattata g 621

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<210> 315
 <211> 606
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<400> 315
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cccagattcc agaggggtga ctacatatt gatgtctgta tcaatgacta cctggatgtt 180
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gaatgtaacc ggcctcactc tccaaatgga ccgctgaagt tctctgaaaa attccagctc 360
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tctgcaatcc cagataatgg aagaaggctc tgtctaaagc tcaaagtctt tgtgagacca 480
acaaatgaca ccgtacatga gtcagccgag ccacccogcg gcgagaacgc ggcacaaaca 540
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 <211> 718
 <212> DNA
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<220>
 <223> A novel predicted alternative spliced variant

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aactacatca aatgggtctt tggagggcct ggataaccag gagggagggg tgtgccagac 180
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aacaagtccc ttgtgaaac caaatccagg ttctagcaca gacggcaaca gcgccggaca 360
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catcatcttc atcgatcatca tcatcacgct ggtggtcctc ttgctgaagt accggaggag 480
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caagcgacgc ggcaacaaca acggctcaga gccagtgac attatcatcc cgctaaggac 600
tgccgacagc gtcttctgcc ctcaactaga gaaggtcagc ggggactacg ggcacccggc 660
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<210> 317
<211> 909
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

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aaggtctga 909

<210> 318
<211> 888
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 318
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<210> 319

<211> 2893

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 319

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 <211> 2297
 <212> DNA
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<220>
 <223> A novel predicted alternative spliced variant

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 gaatggttcc cgtctga 2297

<210> 321

<211> 2805

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 321

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 aataactggc taogaactga ttggatcacc cgagaagggg ctcagagggt gtatattgag 300

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<212> DNA
<213> Artificial sequence

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<220>
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<211> 2778

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 324

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<211> 3011

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 325

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<211> 3046

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 326

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<210> 327

<211> 2904

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 327

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 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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 <211> 2958
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<210> 330
 <211> 2871
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<223> A novel predicted alternative spliced variant

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<220>

<223> A novel predicted alternative spliced variant

<400> 342

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<210> 344

<211> 2780

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 344

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<211> 3652

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 345

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<211> 3852

<212> DNA

<213> Artificial sequence

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<223> A novel predicted alternative spliced variant

<400> 351

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<210> 354

<211> 1879

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 354

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<210> 355

<211> 1811

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 355

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<210> 356

<211> 1835

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 356

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<210> 357

<211> 1863

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant.

<400> 357

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<210> 358

<211> 1811

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 358

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<210> 359
<211> 675
<212> DNA
<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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<210> 360
<211> 585
<212> DNA
<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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<210> 361
<211> 675
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

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<210> 362
<211> 1634
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

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<210> 363
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 <212> DNA
 <213> Artificial sequence

<220>
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<212> DNA

<213> Artificial sequence

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<223> A novel predicted alternative spliced variant

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<212> DNA

<213> Artificial sequence

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<223> A novel predicted alternative spliced variant

<400> 366

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<212> DNA

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<223> A novel predicted alternative spliced variant

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<220>
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<211> 2409

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 374

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<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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<210> 376

<211> 1314

<212> DNA

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant

<400> 376

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<210> 378
 <211> 3626
 <212> DNA
 <213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 378

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<210> 379

<211> 3633

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 379

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cagctcgtgc agccatctgg gggcctccag gcttcagtca tctccaacat cgtgctgatg 660
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<210> 380
<211> 643
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 380
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cctgggcttg gggatgccct gcggggtgta cccccccgt tgcggctcgg gcctgcgctg 240
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gtgctggtgt gtggaccgga agacgggggt gaagcttcg gggggcctgg agccaaagg 600
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<210> 381
<211> 2616
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 381
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ggaaagtctt gtggaaagat agccctcct cctgttgtgt cticagggcc atttcttttt 360
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aaactgaata cacagagtac ttattcggag gcatga

2616

<210> 382
<211> 523
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 382
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gaagcagggg ggctcccag ggaacccga gtcacggact tggatcattt aaaggggatt 180
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attcagagaa cagttcgaag aaaactggta taatacgtac tcgtcaaacc tatataagca 360
cgtggacact ggaagggcat actatgttgc attaaataaa gatgggaccc cgagagaagg 420
gactaggact aaacggcacc agaaattcac acatttttta cctagaccag tggacccga 480
caaagtacct gaactgtata aggatattct aagccaaagt tga 523

<210> 383
<211> 523
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 383
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tccagcggg gaaggcatgt gcggagctac aatcaccttc aaggagatgt ccgctggaga 240
aagctattct ctttcaccaa gtactttctc aagattgaga agaacgggaa ggtcagcggg 300
accaagaagg agaactgccc gtacaaaaga atttaacaat gactgttaagc tgaaggagag 360
gatagaggaa aatggatata atacctatgc atcatttaac tggcagcata atgggaggca 420
aatgtatgtg gcattgaatg gaaaaggagc tccaaggaga ggacagaaaa cacgaaggaa 480
aaacacctct gctcactttc ttccaatggg ggtacactca tag 523

<210> 384
<211> 587
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 384
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atttcataaa gcgctacccc aaggggcagc cggagcttca gaagcccttc aagtacacga 540
cggtgaccaa gaggtcccgt cggatccggc ccacacaccc tgcctag 587

<210> 385
<211> 517
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 385
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<210> 386
<211> 1369
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 386
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<210> 387
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 <212> DNA
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<220>
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<210> 388
 <211> 1366
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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 cagtacaaca caaacgctct gcagagagat gctccacacg tggaaaccga tttctcttcc 240
 cagaaacttc aacatctgga acatgtgatg gaaaattata ctcaaggctt gcaaaaactt 300
 gagaattaca ttgtggaaaa catgaagtcg gagatggccc agatacagca gaatgcagtt 360
 cagaaccaca cggctaccat gctggagata ggaaccagcc tctctctca gactgcagag 420
 cagaccagaa agctgacaga tgttgagacc caggtactaa atcaaaactt tcgacttgag 480
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<210> 389
 <211> 1124
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<210> 390

<211> 2226

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 390

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<210> 391

<211> 2211

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 391

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<210> 392

<211> 2109

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 392

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<210> 393
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 <212> DNA
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<220>
 <223> A novel predicted alternative spliced variant

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<210> 394

<211> 2220

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 394

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<210> 395

<211> 2187

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 395

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<210> 396

<211> 3022

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 396
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<210> 397

<211> 1775

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 397

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<210> 398

<211> 2233

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 398

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<210> 399
 <211> 2249
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<210> 400

<211> 1517

<212> DNA

<213> Artificial sequence.

<220>

<223> A novel predicted alternative spliced variant

<400> 400

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<210> 401

<211> 1607

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 401

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 gctggagaca ggagaccctt gctgttagac agagctgcag gtttgaagga aaagaccctg 180
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<210> 402

<211> 1731

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 402

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 gctggagaca ggagaccctt gcctgtagac agagctgcag gtttgaagga aaagaccctg 180
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<210> 403
<211> 1685
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 403
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attctacttg atgtgagcac caagaacca gtcaggacag tcaatgagaa cttcctctct 240
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gataa 1685

<210> 404
<211> 1672
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 404
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 gtccaagtca gtgcaactga atggccagcc cttagtgatg gtggacgacg ggaccctccc 1560
 agaattgaag ccccgccccc ttggggcggg ccggacattg gtcacccctc cagtcaccat 1620
 gggctttttt gtggccaaga atgtcaatgc tttggcctgc cgctaccgat aa 1672

<210> 405

<211> 1664

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 405

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agccccgcc ccttcggggc ggccggacat tggtcacccc tcagtcacc atgggctttt 1620
ttgtgggtcaa gaatgtcaat gctttggcct gccgctaccg ataa 1664

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<210> 406

<211> 1633

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 406

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ccgctaccga taa 1633

<210> 407
<211> 1632
<212> DNA
<213> Artificial sequence

<220>
<223> A novel predicted alternative spliced variant

<400> 407
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<210> 408

<211> 2091

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 408

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 ggcaatttca ggattattgg gactttgcag aactctgcag agttttcaga agcctttcac 2040
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<210> 409

<211> 2134

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 409

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<210> 410

<211> 2118

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 410

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 aagtgcgggg tttggtga 2118

<210> 411
 <211> 2116
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<210> 412

<211> 2253

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 412

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<210> 413

<211> 2149

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 413

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 caatttcagg attattggga ctttgcagaa ctctgcagag ttttcagaag cttttactg 2100
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<210> 414

<211> 1951

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 414

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gcccaaacgg ctgggggccc ataccctatg a 1951

<210> 415

<211> 1977

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 415

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gagccaggcc ctgccaatgc caagtggcta aaagagggcc agaaccagct cgggcgggcc 240
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<210> 416

<211> 1999

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 416

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 gggggcccat. accccatga 1999

<210> 417

<211> 2042

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 417

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<210> 418

<211> 2011

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 418

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<210> 419

<211> 485

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 419

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ccattaaaag actgaaaagg tcaccagata aacaaatggc agtgcttcct agaagagagc 120

ggaatcggca ggctgcaggt gccaacccag agaattccag aggaaaaggt cggagaggcc 180

agaggggcaa aaacgggggt tgtgtcttaa ctgcaatata tttaaagtgc actgacttgg 240

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 gtgacaaagt agggcaggca tgttgacagc ccatcgccct tgatgatgac ctgtcgtttt 420
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 tctga 485

<210> 420
 <211> 1231
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

<400> 420
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<210> 421
 <211> 751
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

<400> 421
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 catatcacac aactggctct cagccataac aagctaaca tgggtgccacc gaacatcgca 180

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<210> 422
 <211> 1467
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

<400> 422
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<213> Artificial sequence

<220>
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<212> DNA
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<211> 6045

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 425

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<211> 1569

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 427

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<210> 428

<211> 1904

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 428

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<210> 429

<211> 1937

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 429

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<210> 430

<211> 2016

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 430

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 gaagggtgact tgggaaattt ctctgttat gttgaaaatg gaaatggacg tcgacacgcc 960
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 cagcatacct actgtaacat ccctatgaca ctcacaaag ggcagcggcc acagacaaaa 1920
 tcgagcaggg agcagaatcc agatgaggcc cacacaaaca gtgccatcct gccgctgttG 1980
 ccaagggaga ccagtatatc cagtgtgata tggTga 2016

<210> 431

<211> 1958

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 431

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 tatcaagttt tggTgggaga gcctgttTga atcaaatgtg cactctttta tggttatata 180
 agaacaaatt actcccttgc ccaaagtgtt ggactcagtt tgatgtggta caaagtTct 240
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 ctgcttataa gagaagtcag agaagatgac attggaaatt atacctgtga attaaaatat 660
 ggaggctttg ttgtgagaag aactactgaa ttaactgtta cagcccctct gactgataag 720
 ccaccaagc tttgtatcc tatggaaagt aaactgacaa ttcaggagac ccagctggaa 780
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 atcagcatac ctactgtaac atccctatga cactcatcaa cgggcagcgg ccacagacaa 1860
 aatcagcag ggagcagaat ccagatgagg cccacacaaa cagtgccatc ctgccgctgt 1920
 tgccaaggga gaccagtata tccagtgtga tatgggtga 1958

<210> 432

<211> 1945

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 432

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 tatcaagttt tgggtggaga gcctgttctga atcaaatgtg cactcttita tggttatata 180
 agaacaaatt actcccttgc ccaagtgctt ggactcagtt tgatgtggta caaaagttct 240
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 ggactctgct ataattccaa gatgaagtat ttgaaaaag ctgaacttag caaaagcaag 480
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 ctgcttataa gagaagtcag agaagatgac attggaaatt atacctgtga attaaaatat 660
 ggaggccttg ttgtgagaag aactactgaa ttaactgtta cagccctctt gactgataag 720
 ccaccaagc ttttgtatcc tatggaaagt aaactgacaa ttcaggagac ccagctgggt 780
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 ctgtaacatc cctatgacac tcatcaacgg gcagcggcca cagacaaaat cgagcaggga 1860
 gcagaatcca gatgaggccc acacaaacag tgccatcctg ccgctgttgc caagggagac 1920
 cagtatatcc agtgtgatat ggtga 1945

<210> 433

<211> 1874

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 433

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 tacatggctt tggcaggatg accagtcgga gtgaaatgtg cccttttcta cagttatatt 180
 cgtaccaact atagcacggc ccagagcact gggctcaggc ttatgtggta caaaaacaaa 240
 ggtgatattg aagagoccat catcttttca gaggtcaggga tgagcaaaga ggaagattca 300
 atatggtttc actcagctga ggcacaagac agtggattct acacttgtgt ttaaggaat 360

gcaagccaaa aatgtggaga agcataataa tacagaaagg aaatgctctt ctgatccaag 420
 aagttcaaga agaagatgga ggaattaca catgtgaact taaatatgaa ggaaaacttg 480
 taagacgaac aactgaattg aaagttacag ctttactcac agacaagcct cccaagccat 540
 tgttcccat ggagaatcag ccaagtgtta tagatgtcca gctgggtaag cctctgaaca 600
 tcccctgcaa agcattcttc ggattcagtg gagagtctgg gccaatgac tactggatga 660
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 acctgcctct gacgtactc aacggacagc tacccttaa taacacctg aaagataccc 1800
 aggaatttca caggaacagt tctttgtgac ctttatoctc caaagagctt agctttacca 1860
 gtgatatttg gtag 1874

<210> 434

<211> 1907

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 434

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tgctacaaca gcaggatccg ctatttagaa aaatctgaag tcactaaaag aaaggagatc 480
tcctgtccag acatggatga ctttaaaaag tccgatcagg agcctgatgt tgtgtggtat 540
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ttatagatgt ccagctgggt aagcctctga acatcccctg caaagcattc ttcggattca 660
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agctaccctt taataacacc ctgaaagata ccaggaatt tcacaggaac agttctttgc 1860
tgccctttatc ctcaaagag cttagcttta ccagtgatat ttggtag 1907

<210> 435

<211> 1986

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 435

atgaagccac catttctttt ggccttctg gtctgttctg tagtcagcac aaatctgaag 60
atgggtgtcaa agagaaattc tgtggatggc tgcattgact ggtcagtga tctcaagaca 120
tacatggctt tggcaggtga accagtcga gtgaaatgtg cctttttcta cagttatatt 180
cgtaccaact atagcacggc ccagagcact gggctcaggc ttatgtggta caaaaacaaa 240
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tcaacatatt gcatgaaggt gtcaatgtcc ttgactgttg cagagaatga atcaggcctg 420
tgctacaaca gcaggatccg ctatttagaa aaatctgaag tcactaaaag aaaggagatc 480
tcctgtccag acatggatga ctttaaaaag tccgatcagg agcctgatgt tgtgtggtat 540

aaggaatgca agccaaaaat gtggagaagc ataataatac agaaaggaaa tgctcttctg 600
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 ccagccacga ccttgccagt accttcccta ggcaaccacc atacttattg taacctgcct 1860
 ctgacgctac tcaacggaca gctaccctt aataacaccc tgaaagatac ccaggaattt 1920
 cacaggaaca gttctttgct gcctttatcc tccaaagac ttagctttac cagtgtatatt 1980
 tggtag 1986

<210> 436

<211> 1931

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 436

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 tacatggcctt tggcagggtga accagtcoga gtgaaatgtg cccttttcta cagttatatt 180
 cgtaccaact atagcacggc ccagagcact gggctcaggc ttatgtggta caaaaacaaa 240
 ggtgatttgg aagagcccat catcttttca gaggtcagga tgagcaaaga ggaagattca 300
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 tgctacaaca gcaggatccg ctatttagaa aaatctgaag tcaactaaaag aaaggagatc 480

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tgctcttgac gctactcaac ggacagctac cccttaataa caccctgaaa gatacccagg 1860
aatttcacag gaacagttct ttgtgcctt tatcctccaa agagcttagc tttaccagtg 1920
atatttggtg g 1931

<210> 437

<211> 1915

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 437

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tcaacatatt gcatgaaggt gtcattgtcc ttgactgttg cagagaatga atcaggcctg 420
tgctacaaca gcaggatccg ctatttagaa aaatctgaag tcactaaaag aaaggagatc 480
tcctgtccag acatggatga ctttaaaaag tccgatcagg agcctgatgt tgtgtggtat 540

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<211> 3437

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 438

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<210> 439

<211> 3419

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

<400> 439

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<210> 440

<211> 3336

<212> DNA

<213> Artificial sequence

<220>

<223> A novel predicted alternative spliced variant

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 <211> 3360
 <212> DNA
 <213> Artificial sequence

<220>
 <223> A novel predicted alternative spliced variant

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<213> Artificial sequence

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 <211> 984
 <212> PRT
 <213> Homo sapiens

<400> 452

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 Asp Glu Asn Leu Asn Thr Ile Arg Thr Tyr Gln Val Cys Asn Val Phe
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 Glu Pro Asn Gln Asn Asn Trp Leu Leu Thr Thr Phe Ile Asn Arg Arg
 65 70 75 80
 Gly Ala His Arg Ile Tyr Thr Glu Met Arg Phe Thr Val Arg Asp Cys
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 Ser Ser Leu Pro Asn Val Pro Gly Ser Cys Lys Glu Thr Phe Asn Leu
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 Tyr Tyr Tyr Glu Thr Asp Ser Val Ile Ala Thr Lys Lys Ser Ala Phe
 115 120 125
 Trp Ser Glu Ala Pro Tyr Leu Lys Val Asp Thr Ile Ala Ala Asp Glu
 130 135 140
 Ser Phe Ser Gln Val Asp Phe Gly Gly Arg Leu Met Lys Val Asn Thr
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 Glu Val Arg Ser Phe Gly Pro Leu Thr Arg Asn Gly Phe Tyr Leu Ala
 165 170 175
 Phe Gln Asp Tyr Gly Ala Cys Met Ser Leu Leu Ser Val Arg Val Phe
 180 185 190
 Phe Lys Lys Cys Pro Ser Ile Val Gln Asn Phe Ala Val Phe Pro Glu
 195 200 205
 Thr Met Thr Gly Ala Glu Ser Thr Ser Leu Val Ile Ala Arg Gly Thr
 210 215 220

Cys Ile Pro Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr Cys
 225 230 235 240
 Asn Gly Asp Gly Glu Trp Met Val Pro Ile Gly Arg Cys Thr Cys Lys
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 Pro Gly Tyr Glu Pro Glu Asn Ser Val Ala Cys Lys Ala Cys Pro Ala
 260 265 270
 Gly Thr Phe Lys Ala Ser Gln Glu Ala Glu Gly Cys Ser His Cys Pro
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 Ser Asn Ser Arg Ser Pro Ala Glu Ala Ser Pro Ile Cys Thr Cys Arg
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 Thr Gly Tyr Tyr Arg Ala Asp Phe Asp Pro Pro Glu Val Ala Cys Thr
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 Asp Val Thr Tyr Asn Ile Ile Cys Lys Lys Cys Arg Ala Asp Arg Arg
 355 360 365
 Ser Cys Ser Arg Cys Asp Asp Asn Val Glu Phe Val Pro Arg Gln Leu
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 385 390 395 400
 Pro Tyr Thr Phe Asp Ile Gln Ala Ile Asn Gly Val Ser Ser Lys Ser
 405 410 415
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 420 425 430
 Ala Pro Ser Thr Val Pro Ile Met His Gln Val Ser Ala Thr Met Arg
 435 440 445
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 450 455 460
 Leu Asp Tyr Glu Ile Arg Tyr Tyr Glu Lys Glu His Asn Glu Phe Asn
 465 470 475 480
 Ser Ser Met Ala Arg Ser Gln Thr Asn Thr Ala Arg Ile Asp Gly Leu
 485 490 495
 Arg Pro Gly Met Val Tyr Val Val Gln Val Arg Ala Arg Thr Val Ala
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 Gly Tyr Gly Lys Phe Ser Gly Lys Met Cys Phe Gln Thr Leu Thr Asp
 515 520 525
 Asp Asp Tyr Lys Ser Glu Leu Arg Glu Gln Leu Pro Leu Ile Ala Gly

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Asp Lys Leu Gln His Tyr Ser Thr Gly Arg Gly Ser Pro Gly Met Lys 580 585 590		
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Glu Phe Ala Lys Glu Ile Asp Val Ser Phe Val Lys Ile Glu Glu Val 610 615 620		
Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Arg Leu Lys Leu 625 630 635 640		
Pro Gly Lys Arg Glu Ile Tyr Val Ala Ile Lys Thr Leu Lys Ala Gly 645 650 655		
Tyr Ser Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met 660 665 670		
Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr 675 680 685		
Lys Ser Arg Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn Gly Ala 690 695 700		
Leu Asp Ser Phe Leu Arg Gln Asn Asp Gly Gln Phe Thr Val Ile Gln 705 710 715 720		
Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala 725 730 735		
Glu Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val 740 745 750		
Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Tyr 755 760 765		
Leu Gln Asp Asp Thr Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly Gly 770 775 780		
Lys Ile Pro Val Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys 785 790 795 800		
Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu 805 810 815		
Val Met Ser Phe Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp 820 825 830		
Val Ile Asn Ala Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro Met Asp 835 840 845		

Cys Pro Ala Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp
850 855 860

Arg Asn Ser Arg Pro Arg Phe Ala Glu Ile Val Asn Thr Leu Asp Lys
865 870 875 880

Met Ile Arg Asn Pro Ala Ser Leu Lys Thr Val Ala Thr Ile Thr Ala
885 890 895

Val Pro Ser Gln Pro Leu Leu Asp Arg Ser Ile Pro Asp Phe Thr Ala
900 905 910

Phe Thr Thr Val Asp Asp Trp Leu Ser Ala Ile Lys Met Val Gln Tyr
915 920 925

Arg Asp Ser Phe Leu Thr Ala Gly Phe Thr Ser Leu Gln Leu Val Thr
930 935 940

Gln Met Thr Ser Glu Asp Leu Leu Arg Ile Gly Ile Thr Leu Ala Gly
945 950 955 960

His Gln Lys Lys Ile Leu Asn Ser Ile His Ser Met Arg Val Gln Ile
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Ser Gln Ser Pro Thr Ala Met Ala
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<210> 453

<211> 3865

<212> DNA

<213> Homo sapiens

<400> 453

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<210> 454

<211> 225

<212> PRT

<213> Homo sapiens

<400> 454

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Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile Leu Leu Ser
 35 40 45

Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro Asp Arg Gly Pro
 50 55 60

Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Phe Cys Arg Gln Gly
 65 70 75 80

Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser Ile Gln Gly Thr Pro Glu
 85 90 95

Asp Thr Ser Ser Phe Thr His Phe Asn Leu Ile Pro Val Gly Leu Arg
 100 105 110

Val Val Thr Ile Gln Ser Ala Lys Leu Gly His Tyr Met Ala Met Asn
 115 120 125

Ala Glu Gly Leu Leu Tyr Ser Ser Pro His Phe Thr Ala Glu Cys Arg
 130 135 140

Phe Lys Glu Cys Val Phe Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala
 145 150 155 160

Leu Tyr Arg Gln Arg Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp
 165 170 175

Lys Glu Gly Gln Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala
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Ala Ala His Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu

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Pro Ser Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala
210 215 220

Pro
225

<210> 455
<211> 2763
<212> DNA
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<210> 456
<211> 873
<212> PRT
<213> Homo sapiens
<400> 456

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Cys Glu Pro Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu
35          40          45

Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Val Asp Gly Ser Asp Glu
50          55          60

Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Asn
65          70          75          80

Asn Gly Gln Cys Val Pro Ser Arg Trp Lys Cys Asp Gly Asp Pro Asp
85          90          95

Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr
100         105         110

Cys Arg Ile His Glu Ile Ser Cys Gly Ala His Ser Thr Gln Cys Ile
115         120         125

Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Ser Gly Glu
130         135         140

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Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Pro Asp Glu Phe Thr
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Cys Ser Ser Gly Arg Cys Ile Ser Arg Asn Phe Val Cys Asn Gly Gln
165 170 175

Asp Asp Cys Ser Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr
180 185 190

Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Ile
195 200 205

Ser Trp Val Cys Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu
210 215 220

Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro
225 230 235 240

Ala Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
245 250 255

Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
260 265 270

Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
275 280 285

Ser Cys Ile His Gly Ser Arg Gln Cys Asn Gly Ile Arg Asp Cys Val
290 295 300

Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
305 310 315 320

Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Ile Ser Lys
325 330 335

Val Cys Asn Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
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His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
370 375 380

Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys
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Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly
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Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly
420 425 430

Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg
435 440 445

Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu
450 455 460

Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala
465 470 475 480

Gln Lys Leu Phe Trp Ala Asp Leu Ser Gln Lys Ala Ile Phe Ser Ala
485 490 495

Ser Ile Asp Asp Lys Val Gly Arg His Val Lys Met Ile Asp Asn Val
500 505 510

Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp Val Tyr Lys Thr Ile Tyr
515 520 525

Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser Val Ala Thr Leu Asp Gly
530 535 540

Thr Lys Arg Lys Phe Leu Phe Asn Ser Asp Leu Arg Glu Pro Ala Ser
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Ile Ala Val Asp Pro Leu Ser Gly Phe Val Tyr Trp Ser Asp Trp Gly
565 570 575

Glu Pro Ala Lys Ile Glu Lys Ala Gly Met Asn Gly Phe Asp Arg Arg
580 585 590

Pro Leu Val Thr Ala Asp Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp
595 600 605

Leu Ile Lys Ser Arg Leu Tyr Trp Leu Asp Ser Lys Leu His Met Leu
610 615 620

Ser Ser Val Asp Leu Asn Gly Gln Asp Arg Arg Ile Val Leu Lys Ser
625 630 635 640

Leu Glu Phe Leu Ala His Pro Leu Ala Leu Thr Ile Phe Glu Asp Arg
645 650 655

Val Tyr Trp Ile Asp Gly Glu Asn Glu Ala Val Tyr Gly Ala Asn Lys
660 665 670

Phe Thr Gly Ser Glu Leu Ala Thr Leu Val Asn Asn Leu Asn Asp Ala
675 680 685

Gln Asp Ile Ile Val Tyr His Glu Leu Val Gln Pro Ser Gly Lys Asn
690 695 700

Trp Cys Glu Glu Asp Met Glu Asn Gly Gly Cys Glu Tyr Leu Cys Leu
705 710 715 720

Pro Ala Pro Gln Ile Asn Asp His Ser Pro Lys Tyr Thr Cys Ser Cys
725 730 735

Pro Ser Gly Tyr Asn Val Glu Glu Asn Gly Arg Asp Cys Gln Ser Thr
740 745 750

Ala Thr Thr Val Thr Tyr Ser Glu Thr Lys Asp Thr Asn Thr Thr Glu

755 760 765
 Ile Ser Ala Thr Ser Gly Leu Val Pro Gly Gly Ile Asn Val Thr Thr
 770 775 780

Ala Val Ser Glu Val Ser Val Pro Pro Lys Gly Thr Ser Ala Ala Trp
 785 790 795 800

Ala Ile Leu Pro Leu Leu Leu Leu Val Met Ala Ala Val Gly Gly Tyr
 805 810 815

Leu Met Trp Arg Asn Trp Gln His Lys Asn Met Lys Ser Met Asn Phe
 820 825 830

Asp Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp
 835 840 845

Ile Gly Arg His Ser Ala Ser Val Gly His Thr Tyr Pro Ala Ile Ser
 850 855 860

Val Val Ser Thr Asp Asp Asp Leu Ala
 865 870

<210> 457
 <211> 3355.
 <212> DNA
 <213> Homo sapiens

<400> 457
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 gctcgcgctg tgctggggcg cccgggagag cggcgccacc ggaaccggga gaaaagccaa 180
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 atgccgcata catgaaatca gctgtggcgc ccattctact cagtgtatcc cagtgtcctg 480
 gagatgtgat ggtgaaaatg attgtgacag tggagaagat gaagaaaact gtggcaatat 540
 aacatgtagt cccgacgagt tcaacctgtc cagtggccgc tgcactcca ggaactttgt 600
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 ctgtggcgcc catgagttcc agtgcagcac ctctctctgc atccccatca gctgggtatg 720
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 ctgtccctct cgaaattgcc gacctgacca atttgaatgt gaggatggca gctgcacca 960
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cagcagtga aattgtgcta tagtgtatc cacctgtaca tacattgtat aggccatctg 3060
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attaaccag cagcttataa aaaaaaaa aaaaaaaaaa aaaaaaaa aaaa 3355

<210> 458
<211> 695
<212> PRT
<213> Homo sapiens

<400> 458

Met Ala Leu Leu Val Ser Leu Leu Ala Phe Leu Ser Leu Gly Ser
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Gly Cys His His Arg Ile Cys His Cys Ser Asn Arg Val Phe Leu Cys
20 25 30

Gln Glu Ser Lys Val Thr Glu Ile Pro Ser Asp Leu Pro Arg Asn Ala
35 40 45

Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
50 55 60

Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
65 70 75 80

Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
85 90 95

Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn
100 105 110

Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
115 120 125

Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
130 135 140

Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
145 150 155 160

Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
165 170 175

Leu Asn Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly
180 185 190

Thr Gln Leu Asp Glu Leu Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu
195 200 205

Leu Pro Asn Asp Val Phe His Gly Ala Ser Gly Pro Val Ile Leu Asp
210 215 220

Ile Ser Arg Thr Arg Ile His Ser Leu Pro Ser Tyr Gly Leu Glu Asn
225 230 235 240

Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro
245 250 255

Thr Leu Glu Lys Leu Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro
260 265 270

Ser His Cys Cys Ala Phe Ala Asn Trp Arg Arg Gln Ile Ser Glu Leu
275 280 285

His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Tyr Met
290 295 300

Thr Gln Ala Arg Gly Gln Arg Ser Ser Leu Ala Glu Asp Asn Glu Ser
305 310 315 320

Ser Tyr Ser Arg Gly Phe Asp Met Thr Tyr Thr Glu Phe Asp Tyr Asp
325 330 335

Leu Cys Asn Glu Val Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala
340 345 350

Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu
355 360 365

Ile Trp Phe Ile Ser Ile Leu Ala Ile Thr Gly Asn Ile Ile Val Leu
370 375 380

Val Ile Leu Thr Thr Ser Gln Tyr Lys Leu Thr Val Pro Arg Phe Leu
385 390 395 400

Met Cys Asn Leu Ala Phe Ala Asp Leu Cys Ile Gly Ile Tyr Leu Leu
405 410 415

Leu Ile Ala Ser Val Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr
420 425 430

Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe
435 440 445

Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr
450 455 460

Leu Glu Arg Trp His Thr Ile Thr His Ala Met Gln Leu Asp Cys Lys
465 470 475 480

Val Gln Leu Arg His Ala Ala Ser Val Met Val Met Gly Trp Ile Phe
485 490 495

Ala Phe Ala Ala Ala Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met
500 505 510

Lys Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln
515 520 525

Leu Tyr Val Met Ser Leu Leu Val Leu Asn Val Leu Ala Phe Val Val
530 535 540

Ile Cys Gly Cys Tyr Ile His Ile Tyr Leu Thr Val Arg Asn Pro Asn
545 550 555 560

Ile Val Ser Ser Ser Ser Asp Thr Arg Ile Ala Lys Arg Met Ala Met
565 570 575

Leu Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala
580 585 590

Ile Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys
595 600 605

Ile Leu Leu Val Leu Phe His Pro Ile Asn Ser Cys Ala Asn Pro Phe
610 615 620

Leu Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu
625 630 635 640

Leu Ser Lys Cys Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr
645 650 655

Glu Thr Ser Ser Thr Val His Asn Thr His Pro Arg Asn Gly His Cys
660 665 670

Ser Ser Ala Pro Arg Val Thr Ser Gly Ser Thr Tyr Ile Leu Val Pro
675 680 685

Leu Ser His Leu Ala Gln Asn
690 695

<210> 459
<211> 2382
<212> DNA
<213> Homo sapiens

<400> 459
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caggatgtca tcatcggatc tgtcactgct ctaacagggt ttttctctgc caagagagca 180
aggtagacaga gattccttct gacctccga ggaatgccat tgaactgagg tttgtcctca 240
ccaagcttcg agtcatccaa aaagggtgcat tttcaggatt tggggacctg gagaaaatag 300
agatctctca gaatgatgtc ttggagggtga tagaggcaga tgtgttctcc aaccttccca 360
aattacatga aattagaatt gaaaaggcca acaacctgct ctacatcaac cctgaggcct 420
tccagaacct tcccaacctt caatatctgt taatatccaa cacaggatt aagcaccttc 480
cagatgttca caagattcat tctctccaaa aagttttact tgacattcaa gataacataa 540
acatccacac aattgaaaga aattctttcg tggggctgag ctttgaaagt gtgattctat 600
ggctgaataa gaatgggatt caagaaatac acaactgtgc attcaatgga acccaactag 660
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gagcctctgg accagtcatt ctgatatatt caagaacaag gatccattcc ctgcctagct 780
atggcttaga aaatcttaag aagctgaggg ccaggctcgac ttacaactta aaaaagctgc 840
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ggcaaaactgg ggcaggatgt gatgctgctg gctttttcac tgtctttgcc agtgagctgt 1440
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ttgcttttgc agctgccctc tttcccatct ttggcatcag cagctacatg aaggtgagca 1620
tctgctgccc catggatatt gacagccett tgtcacagct gtatgtcatg tccctccttg 1680
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atttcttcat tctgctgagc aagtgtggct gctatgaaat gcaagcccaa atttatagga 2040
cagaaacttc atccactgtc cacaacaccc atccaaggaa tggccactgc tcttcagctc 2100
ccagagtcc cagtgggttc acttacatac ttgtccctct aagtcattta gcccaaaact 2160
aaaacacaat gtgaaaatgt atctgagtat tgaatgataa ttcagtcctg cctttgaagg 2220
gtatgtcaca aagagctgac agtggttcta cacatttcat ctaatttaat attcctggca 2280
tacctttaag gtaaatgggt caggaaactat taattccatg tgatacatta ggaagctgaa 2340
ttattagtaa caacaataat aattaaagaa tgcaatactg ta 2382

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<210> 460
<211> 2471
<212> PRT
<213> Homo sapiens
<400> 460

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Met Pro Ala Leu Arg Pro Ala Leu Leu Trp Ala Leu Leu Ala Leu Trp
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Leu Cys Cys Ala Ala Pro Ala His Ala Leu Gln Cys Arg Asp Gly Tyr
20 25 30

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Glu Pro Cys Val Asn Glu Gly Met Cys Val Thr Tyr His Asn Gly Thr
35 40 45

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Gly Tyr Cys Lys Cys Pro Glu Gly Phe Leu Gly Glu Tyr Cys Gln His
50 55 60

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Arg Asp Pro Cys Glu Lys Asn Arg Cys Gln Asn Gly Gly Thr Cys Val
65 70 75 80

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Ala Gln Ala Met Leu Gly Lys Ala Thr Cys Arg Cys Ala Ser Gly Phe
85 90 95

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Thr Gly Glu Asp Cys Gln Tyr Ser Thr Ser His Pro Cys Phe Val Ser
100 105 110

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Arg Pro Cys Leu Asn Gly Gly Thr Cys His Met Leu Ser Arg Asp Thr
115 120 125

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Tyr Glu Cys Thr Cys Gln Val Gly Phe Thr Gly Lys Glu Cys Gln Trp
130 135 140

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Thr Asp Ala Cys Leu Ser His Pro Cys Ala Asn Gly Ser Thr Cys Thr
145 150 155 160

Thr Val Ala Asn Gln Phe Ser Cys Lys Cys Leu Thr Gly Phe Thr Gly
165 170 175

Gln Lys Cys Glu Thr Asp Val Asn Glu Cys Asp Ile Pro Gly His Cys
180 185 190

Gln His Gly Gly Thr Cys Leu Asn Leu Pro Gly Ser Tyr Gln Cys Gln
195 200 205

Cys Pro Gln Gly Phe Thr Gly Gln Tyr Cys Asp Ser Leu Tyr Val Pro
210 215 220

Cys Ala Pro Ser Pro Cys Val Asn Gly Gly Thr Cys Arg Gln Thr Gly
225 230 235 240

Asp Phe Thr Phe Glu Cys Asn Cys Leu Pro Gly Phe Glu Gly Ser Thr
245 250 255

Cys Glu Arg Asn Ile Asp Asp Cys Pro Asn His Arg Cys Gln Asn Gly
260 265 270

Gly Val Cys Val Asp Gly Val Asn Thr Tyr Asn Cys Arg Cys Pro Pro
275 280 285

Gln Trp Thr Gly Gln Phe Cys Thr Glu Asp Val Asp Glu Cys Leu Leu
290 295 300

Gln Pro Asn Ala Cys Gln Asn Gly Gly Thr Cys Ala Asn Arg Asn Gly
305 310 315 320

Gly Tyr Gly Cys Val Cys Val Asn Gly Trp Ser Gly Asp Asp Cys Ser
325 330 335

Glu Asn Ile Asp Asp Cys Ala Phe Ala Ser Cys Thr Pro Gly Ser Thr
340 345 350

Cys Ile Asp Arg Val Ala Ser Phe Ser Cys Met Cys Pro Glu Gly Lys
355 360 365

Ala Gly Leu Leu Cys His Leu Asp Asp Ala Cys Ile Ser Asn Pro Cys
370 375 380

His Lys Gly Ala Leu Cys Asp Thr Asn Pro Leu Asn Gly Gln Tyr Ile
385 390 395 400

Cys Thr Cys Pro Gln Gly Tyr Lys Gly Ala Asp Cys Thr Glu Asp Val
405 410 415

Asp Glu Cys Ala Met Ala Asn Ser Asn Pro Cys Glu His Ala Gly Lys
420 425 430

Cys Val Asn Thr Asp Gly Ala Phe His Cys Glu Cys Leu Lys Gly Tyr
435 440 445

Ala Gly Pro Arg Cys Glu Met Asp Ile Asn Glu Cys His Ser Asp Pro
450 455 460

Cys Gln Asn Asp Ala Thr Cys Leu Asp Lys Ile Gly Gly Phe Thr Cys
465 470 475 480

Leu Cys Met Pro Gly Phe Lys Gly Val His Cys Glu Leu Glu Ile Asn
485 490 495

Glu Cys Gln Ser Asn Pro Cys Val Asn Asn Gly Gln Cys Val Asp Lys
500 505 510

Val Asn Arg Phe Gln Cys Leu Cys Pro Pro Gly Phe Thr Gly Pro Val
515 520 525

Cys Gln Ile Asp Ile Asp Asp Cys Ser Ser Thr Pro Cys Leu Asn Gly
530 535 540

Ala Lys Cys Ile Asp His Pro Asn Gly Tyr Glu Cys Gln Cys Ala Thr
545 550 555 560

Gly Phe Thr Gly Val Leu Cys Glu Glu Asn Ile Asp Asn Cys Asp Pro
565 570 575

Asp Pro Cys His His Gly Gln Cys Gln Asp Gly Ile Asp Ser Tyr Thr
580 585 590

Cys Ile Cys Asn Pro Gly Tyr Met Gly Ala Ile Cys Ser Asp Gln Ile
595 600 605

Asp Glu Cys Tyr Ser Ser Pro Cys Leu Asn Asp Gly Arg Cys Ile Asp
610 615 620

Leu Val Asn Gly Tyr Gln Cys Asn Cys Gln Pro Gly Thr Ser Gly Val
625 630 635 640

Asn Cys Glu Ile Asn Phe Asp Asp Cys Ala Ser Asn Pro Cys Ile His
645 650 655

Gly Ile Cys Met Asp Gly Ile Asn Arg Tyr Ser Cys Val Cys Ser Pro
660 665 670

Gly Phe Thr Gly Gln Arg Cys Asn Ile Asp Ile Asp Glu Cys Ala Ser
675 680 685

Asn Pro Cys Arg Lys Gly Ala Thr Cys Ile Asn Gly Val Asn Gly Phe
690 695 700

Arg Cys Ile Cys Pro Glu Gly Pro His His Pro Ser Cys Tyr Ser Gln
705 710 715 720

Val Asn Glu Cys Leu Ser Asn Pro Cys Ile His Gly Asn Cys Thr Gly
725 730 735

Gly Leu Ser Gly Tyr Lys Cys Leu Cys Asp Ala Gly Trp Val Gly Ile
740 745 750

Asn Cys Glu Val Asp Lys Asn Glu Cys Leu Ser Asn Pro Cys Gln Asn

755 760 765
Gly Gly Thr Cys Asp Asn Leu Val Asn Gly Tyr Arg Cys Thr Cys Lys
770 775 780
Lys Gly Phe Lys Gly Tyr Asn Cys Gln Val Asn Ile Asp Glu Cys Ala
785 790 795 800
Ser Asn Pro Cys Leu Asn Gln Gly Thr Cys Phe Asp Asp Ile Ser Gly
805 810 815
Tyr Thr Cys His Cys Val Leu Pro Tyr Thr Gly Lys Asn Cys Gln Thr
820 825 830
Val Leu Ala Pro Cys Ser Pro Asn Pro Cys Glu Asn Ala Ala Val Cys
835 840 845
Lys Glu Ser Pro Asn Phe Glu Ser Tyr Thr Cys Leu Cys Ala Pro Gly
850 855 860
Trp Gln Gly Gln Arg Cys Thr Ile Asp Ile Asp Glu Cys Ile Ser Lys
865 870 875 880
Pro Cys Met Asn His Gly Leu Cys His Asn Thr Gln Gly Ser Tyr Met
885 890 895
Cys Glu Cys Pro Pro Gly Phe Ser Gly Met Asp Cys Glu Glu Asp Ile
900 905 910
Asp Asp Cys Leu Ala Asn Pro Cys Gln Asn Gly Gly Ser Cys Met Asp
915 920 925
Gly Val Asn Thr Phe Ser Cys Leu Cys Leu Pro Gly Phe Thr Gly Asp
930 935 940
Lys Cys Gln Thr Asp Met Asn Glu Cys Leu Ser Glu Pro Cys Lys Asn
945 950 955 960
Gly Gly Thr Cys Ser Asp Tyr Val Asn Ser Tyr Thr Cys Lys Cys Gln
965 970 975
Ala Gly Phe Asp Gly Val His Cys Glu Asn Asn Ile Asn Glu Cys Thr
980 985 990
Glu Ser Ser Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser
995 1000 1005
Phe Ser Cys Leu Cys Pro Val Gly Phe Thr Gly Ser Phe Cys Leu
1010 1015 1020
His Glu Ile Asn Glu Cys Ser Ser His Pro Cys Leu Asn Glu Gly
1025 1030 1035
Thr Cys Val Asp Gly Leu Gly Thr Tyr Arg Cys Ser Cys Pro Leu
1040 1045 1050
Gly Tyr Thr Gly Lys Asn Cys Gln Thr Leu Val Asn Leu Cys Ser
1055 1060 1065

Arg Ser Pro Cys Lys Asn Lys Gly Thr Cys Val Gln Lys Lys Ala
 1070 1075 1080
 Glu Ser Gln Cys Leu Cys Pro Ser Gly Trp Ala Gly Ala Tyr Cys
 1085 1090 1095
 Asp Val Pro Asn Val Ser Cys Asp Ile Ala Ala Ser Arg Arg Gly
 1100 1105 1110
 Val Leu Val Glu His Leu Cys Gln His Ser Gly Val Cys Ile Asn
 1115 1120 1125
 Ala Gly Asn Thr His Tyr Cys Gln Cys Pro Leu Gly Tyr Thr Gly
 1130 1135 1140
 Ser Tyr Cys Glu Glu Gln Leu Asp Glu Cys Ala Ser Asn Pro Cys
 1145 1150 1155
 Gln His Gly Ala Thr Cys Ser Asp Phe Ile Gly Gly Tyr Arg Cys
 1160 1165 1170
 Glu Cys Val Pro Gly Tyr Gln Gly Val Asn Cys Glu Tyr Glu Val
 1175 1180 1185
 Asp Glu Cys Gln Asn Gln Pro Cys Gln Asn Gly Gly Thr Cys Ile
 1190 1195 1200
 Asp Leu Val Asn His Phe Lys Cys Ser Cys Pro Pro Gly Thr Arg
 1205 1210 1215
 Gly Leu Leu Cys Glu Glu Asn Ile Asp Asp Cys Ala Arg Gly Pro
 1220 1225 1230
 His Cys Leu Asn Gly Gly Gln Cys Met Asp Arg Ile Gly Gly Tyr
 1235 1240 1245
 Ser Cys Arg Cys Leu Pro Gly Phe Ala Gly Glu Arg Cys Glu Gly
 1250 1255 1260
 Asp Ile Asn Glu Cys Leu Ser Asn Pro Cys Ser Ser Glu Gly Ser
 1265 1270 1275
 Leu Asp Cys Ile Gln Leu Thr Asn Asp Tyr Leu Cys Val Cys Arg
 1280 1285 1290
 Ser Ala Phe Thr Gly Arg His Cys Glu Thr Phe Val Asp Val Cys
 1295 1300 1305
 Pro Gln Met Pro Cys Leu Asn Gly Gly Thr Cys Ala Val Ala Ser
 1310 1315 1320
 Asn Met Pro Asp Gly Phe Ile Cys Arg Cys Pro Pro Gly Phe Ser
 1325 1330 1335
 Gly Ala Arg Cys Gln Ser Ser Cys Gly Gln Val Lys Cys Arg Lys
 1340 1345 1350

Gly Glu Gln Cys Val His Thr Ala Ser Gly Pro Arg Cys Phe Cys
 1355 1360 1365
 Pro Ser Pro Arg Asp Cys Glu Ser Gly Cys Ala Ser Ser Pro Cys
 1370 1375 1380
 Gln His Gly Gly Ser Cys His Pro Gln Arg Gln Pro Pro Tyr Tyr
 1385 1390 1395
 Ser Cys Gln Cys Ala Pro Pro Phe Ser Gly Ser Arg Cys Glu Leu
 1400 1405 1410
 Tyr Thr Ala Pro Pro Ser Thr Pro Pro Ala Thr Cys Leu Ser Gln
 1415 1420 1425
 Tyr Cys Ala Asp Lys Ala Arg Asp Gly Val Cys Asp Glu Ala Cys
 1430 1435 1440
 Asn Ser His Ala Cys Gln Trp Asp Gly Gly Asp Cys Ser Leu Thr
 1445 1450 1455
 Met Glu Asn Pro Trp Ala Asn Cys Ser Ser Pro Leu Pro Cys Trp
 1460 1465 1470
 Asp Tyr Ile Asn Asn Gln Cys Asp Glu Leu Cys Asn Thr Val Glu
 1475 1480 1485
 Cys Leu Phe Asp Asn Phe Glu Cys Gln Gly Asn Ser Lys Thr Cys
 1490 1495 1500
 Lys Tyr Asp Lys Tyr Cys Ala Asp His Phe Lys Asp Asn His Cys
 1505 1510 1515
 Asp Gln Gly Cys Asn Ser Glu Glu Cys Gly Trp Asp Gly Leu Asp
 1520 1525 1530
 Cys Ala Ala Asp Gln Pro Glu Asn Leu Ala Glu Gly Thr Leu Val
 1535 1540 1545
 Ile Val Val Leu Met Pro Pro Glu Gln Leu Leu Gln Asp Ala Arg
 1550 1555 1560
 Ser Phe Leu Arg Ala Leu Gly Thr Leu Leu His Thr Asn Leu Arg
 1565 1570 1575
 Ile Lys Arg Asp Ser Gln Gly Glu Leu Met Val Tyr Pro Tyr Tyr
 1580 1585 1590
 Gly Glu Lys Ser Ala Ala Met Lys Lys Gln Arg Met Thr Arg Arg
 1595 1600 1605
 Ser Leu Pro Gly Glu Gln Glu Gln Glu Val Ala Gly Ser Lys Val
 1610 1615 1620
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Asp Val Asn Ala Val Asp Asp 1970	His Gly Lys Ser 1975	Ala Leu His Trp 1980
Ala Ala Ala Val Asn Asn Val 1985	Glu Ala Thr Leu 1990	Leu Leu Lys 1995
Asn Gly Ala Asn Arg Asp Met 2000	Gln Asp Asn Lys 2005	Glu Glu Thr Pro 2010
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 aagcatctgt caaataggaa acatcacaaa actgagcact cttctgtgca ctagccatag 11160
 ctggtgacaa acagatgggt gctcagggac aagggtgcctt ccaatggaaa tgcgaagtag 11220
 ttgctatagc aagaattggg aactgggata taagtcataa tattaattat gctgttatgt 11280
 aaatgattgg tttgtaacat tccttaagt aaatttctgt agaacttaat atacaggatt 11340
 ataaaaaat attttgtgta taaatttgtt ataagttcac attcatacat ttatttataa 11400
 agtcagttag atatttgaac atgaaaaaaa aaa 11433

<210> 462

<211> 838

<212> PRT

<213> Homo sapiens

<400> 462

Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
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Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala Cys
 20 25 30

Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
 35 40 45

Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val Asp
 50 55 60

Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
 65 70 75 80

Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
 85 90 95

Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
 100 105 110

Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
 115 120 125

Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
 130 135 140

Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
 145 150 155 160

Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
 165 170 175

Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
 180 185 190

Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
 195 200 205

Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro
 210 215 220

Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
 225 230 235 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
 245 250 255

Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
 260 265 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
 275 280 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro

290 295 300
 Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
 305 310 315 320
 Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His Val
 325 330 335
 Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
 340 345 350
 His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
 355 360 365
 Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
 370 375 380
 Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
 385 390 395 400
 Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
 405 410 415
 Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
 420 425 430
 Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu
 435 440 445
 Val Met Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
 450 455 460
 Lys Asp Phe Ser Trp Phe Gly Phe Gly Lys Val Lys Ser Arg Gln Gly
 465 470 475 480
 Val Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
 485 490 495
 Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
 500 505 510
 Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
 515 520 525
 Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr
 530 535 540
 Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu
 545 550 555 560
 Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu
 565 570 575
 Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
 580 585 590
 Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu
 595 600 605

Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val
610 615 620

Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
625 630 635 640

Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala
645 650 655

Glu Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile
660 665 670

Ala Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe
675 680 685

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu
690 695 700

Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr
705 710 715 720

Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
725 730 735

Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val
740 745 750

Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln
755 760 765

Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln
770 775 780

Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu
785 790 795 800

Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Met Arg Lys Asn Ile
805 810 815

Lys Gly Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val
820 825 830

Tyr Leu Asp Ile Leu Gly
835

<210> 463

<211> 4057

<212> DNA

<213> Homo sapiens

<400> 463

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gcaggagcct ggaccacaggc gccggcgggc ggcgtgaggc gccggagccc gcctcggagg 120

tgcataccgg accccattc gcatctaaac aggaatctgc gcccagaga gtcccgagcg 180

ccgccggtcg gtgcccggcg cgcggggcca tgcagcgagc gccgccgcgg agctccgagc 240

agcggtagcg ccccccgtg aagcgggtcg ctatgcggcg accactgtga accctgccgc 300

ctgccggaac actcttcgct ccggaccagc tcagcctctg ataagctgga ctcggcacgc 360
 ccgcaacaag caccgaggag ttaagagagc cgcaagcgca gggaaggcct ccccgcacgc 420
 gtgggggaaa gcggccgggtg cagcgcgggg acaggcactc gggctggcac tggctgctag 480
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<210> 464

<211> 2313

<212> PRT

<213> Homo sapiens

<400> 464

Met Arg Ile Leu Lys Arg Phe Leu Ala Cys Ile Gln Leu Leu Cys Val
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Cys Arg Leu Asp Trp Ala Asn Gly Tyr Tyr Arg Gln Gln Arg Lys Leu
 20 25 30

Val Glu Glu Ile Gly Trp Ser Tyr Thr Gly Ala Leu Asn Gln Lys Asn
 35 40 45

Trp Gly Lys Lys Tyr Pro Thr Cys Asn Ser Pro Lys Gln Ser Pro Ile
 50 55 60

Asn Ile Asp Glu Asp Leu Thr Gln Val Asn Val Asn Leu Lys Lys Leu
 65 70 75 80

Lys Phe Gln Gly Trp Asp Lys Thr Ser Leu Glu Asn Thr Phe Ile His
 85 90 95
 Asn Thr Gly Lys Thr Val Glu Ile Asn Leu Thr Asn Asp Tyr Arg Val
 100 105 110
 Ser Gly Gly Val Ser Glu Met Val Phe Lys Ala Ser Lys Ile Thr Phe
 115 120 125
 His Trp Gly Lys Cys Asn Met Ser Ser Asp Gly Ser Glu His Ser Leu
 130 135 140
 Glu Gly Gln Lys Phe Pro Leu Glu Met Gln Ile Tyr Cys Phe Asp Ala
 145 150 155 160
 Asp Arg Phe Ser Ser Phe Glu Glu Ala Val Lys Gly Lys Gly Lys Leu
 165 170 175
 Arg Ala Leu Ser Ile Leu Phe Glu Val Gly Thr Glu Glu Asn Leu Asp
 180 185 190
 Phe Lys Ala Ile Ile Asp Gly Val Glu Ser Val Ser Arg Phe Gly Lys
 195 200 205
 Gln Ala Ala Leu Asp Pro Phe Ile Leu Leu Asn Leu Leu Pro Asn Ser
 210 215 220
 Thr Asp Lys Tyr Tyr Ile Tyr Asn Gly Ser Leu Thr Ser Pro Pro Cys
 225 230 235 240
 Thr Asp Thr Val Asp Trp Ile Val Phe Lys Asp Thr Val Ser Ile Ser
 245 250 255
 Glu Ser Gln Leu Ala Val Phe Cys Glu Val Leu Thr Met Gln Gln Ser
 260 265 270
 Gly Tyr Val Met Leu Met Asp Tyr Leu Gln Asn Asn Phe Arg Glu Gln
 275 280 285
 Gln Tyr Lys Phe Ser Arg Gln Val Phe Ser Ser Tyr Thr Gly Lys Glu
 290 295 300
 Glu Ile His Glu Ala Val Cys Ser Ser Glu Pro Glu Asn Val Gln Ala
 305 310 315 320
 Asp Pro Glu Asn Tyr Thr Ser Leu Leu Val Thr Trp Glu Arg Pro Arg
 325 330 335
 Val Val Tyr Asp Thr Met Ile Glu Lys Phe Ala Val Leu Tyr Gln Gln
 340 345 350
 Leu Asp Gly Glu Asp Gln Thr Lys His Glu Phe Leu Thr Asp Gly Tyr
 355 360 365
 Gln Asp Leu Gly Ala Ile Leu Asn Asn Leu Leu Pro Asn Met Ser Tyr
 370 375 380

Val Leu Gln Ile Val Ala Ile Cys Thr Asn Gly Leu Tyr Gly Lys Tyr
 385 390 395 400
 Ser Asp Gln Leu Ile Val Asp Met Pro Thr Asp Asn Pro Glu Leu Asp
 405 410 415
 Leu Phe Pro Glu Leu Ile Gly Thr Glu Glu Ile Ile Lys Glu Glu Glu
 420 425 430
 Glu Gly Lys Asp Ile Glu Glu Gly Ala Ile Val Asn Pro Gly Arg Asp
 435 440 445
 Ser Ala Thr Asn Gln Ile Arg Lys Lys Glu Pro Gln Ile Ser Thr Thr
 450 455 460
 Thr His Tyr Asn Arg Ile Gly Thr Lys Tyr Asn Glu Ala Lys Thr Asn
 465 470 475 480
 Arg Ser Pro Thr Arg Gly Ser Glu Phe Ser Gly Lys Gly Asp Val Pro
 485 490 495
 Asn Thr Ser Leu Asn Ser Thr Ser Gln Pro Val Thr Lys Leu Ala Thr
 500 505 510
 Glu Lys Asp Ile Ser Leu Thr Ser Gln Thr Val Thr Glu Leu Pro Pro
 515 520 525
 His Thr Val Glu Gly Thr Ser Ala Ser Leu Asn Asp Gly Ser Lys Thr
 530 535 540
 Val Leu Arg Ser Pro His Met Asn Leu Ser Gly Thr Ala Glu Ser Leu
 545 550 555 560
 Asn Thr Val Ser Ile Thr Glu Tyr Glu Glu Glu Ser Leu Leu Thr Ser
 565 570 575
 Phe Lys Leu Asp Thr Gly Ala Glu Asp Ser Ser Gly Ser Ser Pro Ala
 580 585 590
 Thr Ser Ala Ile Pro Phe Ile Ser Glu Asn Ile Ser Gln Gly Tyr Ile
 595 600 605
 Phe Ser Ser Glu Asp Pro Glu Thr Ile Thr Tyr Asp Val Leu Ile Pro
 610 615 620
 Glu Ser Ala Arg Asn Ala Ser Glu Asp Ser Thr Ser Ser Gly Ser Glu
 625 630 635 640
 Glu Ser Leu Lys Asp Pro Ser Met Glu Gly Asn Val Trp Phe Pro Ser
 645 650 655
 Ser Thr Asp Ile Thr Ala Gln Pro Asp Val Gly Ser Gly Arg Glu Ser
 660 665 670
 Phe Leu Gln Thr Asn Tyr Thr Glu Ile Arg Val Asp Glu Ser Glu Lys
 675 680 685
 Thr Thr Lys Ser Phe Ser Ala Gly Pro Val Met Ser Gln Gly Pro Ser

690 695 700
 Val Thr Asp Leu Glu Met Pro His Tyr Ser Thr Phe Ala Tyr Phe Pro
 705 710 715 720
 Thr Glu Val Thr Pro His Ala Phe Thr Pro Ser Ser Arg Gln Gln Asp
 725 730 735
 Leu Val Ser Thr Val Asn Val Val Tyr Ser Gln Thr Thr Gln Pro Val
 740 745 750
 Tyr Asn Gly Glu Thr Pro Leu Gln Pro Ser Tyr Ser Ser Glu Val Phe
 755 760 765
 Pro Leu Val Thr Pro Leu Leu Leu Asp Asn Gln Ile Leu Asn Thr Thr
 770 775 780
 Pro Ala Ala Ser Ser Ser Asp Ser Ala Leu His Ala Thr Pro Val Phe
 785 790 795 800
 Pro Ser Val Asp Val Ser Phe Glu Ser Ile Leu Ser Ser Tyr Asp Gly
 805 810 815
 Ala Pro Leu Leu Pro Phe Ser Ser Ala Ser Phe Ser Ser Glu Leu Phe
 820 825 830
 Arg His Leu His Thr Val Ser Gln Ile Leu Pro Gln Val Thr Ser Ala
 835 840 845
 Thr Glu Ser Asp Lys Val Pro Leu His Ala Ser Leu Pro Val Ala Gly
 850 855 860
 Gly Asp Leu Leu Leu Glu Pro Ser Leu Ala Gln Tyr Ser Asp Val Leu
 865 870 875 880
 Ser Thr Thr His Ala Ala Ser Glu Thr Leu Glu Phe Gly Ser Glu Ser
 885 890 895
 Gly Val Leu Tyr Lys Thr Leu Met Phe Ser Gln Val Glu Pro Pro Ser
 900 905 910
 Ser Asp Ala Met Met His Ala Arg Ser Ser Gly Pro Glu Pro Ser Tyr
 915 920 925
 Ala Leu Ser Asp Asn Glu Gly Ser Gln His Ile Phe Thr Val Ser Tyr
 930 935 940
 Ser Ser Ala Ile Pro Val His Asp Ser Val Gly Val Thr Tyr Gln Gly
 945 950 955 960
 Ser Leu Phe Ser Gly Pro Ser His Ile Pro Ile Pro Lys Ser Ser Leu
 965 970 975
 Ile Thr Pro Thr Ala Ser Leu Leu Gln Pro Thr His Ala Leu Ser Gly
 980 985 990
 Asp Gly Glu Trp Ser Gly Ala Ser Ser Asp Ser Glu Phe Leu Leu Pro
 995 1000 1005

Asp Thr Asp Gly Leu Thr Ala Leu Asn Ile Ser Ser Pro Val Ser
1010 1015 1020

Val Ala Glu Phe Thr Tyr Thr Thr Ser Val Phe Gly Asp Asp Asn
1025 1030 1035

Lys Ala Leu Ser Lys Ser Glu Ile Ile Tyr Gly Asn Glu Thr Glu
1040 1045 1050

Leu Gln Ile Pro Ser Phe Asn Glu Met Val Tyr Pro Ser Glu Ser
1055 1060 1065

Thr Val Met Pro Asn Met Tyr Asp Asn Val Asn Lys Leu Asn Ala
1070 1075 1080

Ser Leu Gln Glu Thr Ser Val Ser Ile Ser Ser Thr Lys Gly Met
1085 1090 1095

Phe Pro Gly Ser Leu Ala His Thr Thr Thr Lys Val Phe Asp His
1100 1105 1110

Glu Ile Ser Gln Val Pro Glu Asn Asn Phe Ser Val Gln Pro Thr
1115 1120 1125

His Thr Val Ser Gln Ala Ser Gly Asp Thr Ser Leu Lys Pro Val
1130 1135 1140

Leu Ser Ala Asn Ser Glu Pro Ala Ser Ser Asp Pro Ala Ser Ser
1145 1150 1155

Glu Met Leu Ser Pro Ser Thr Gln Leu Leu Phe Tyr Glu Thr Ser
1160 1165 1170

Ala Ser Phe Ser Thr Glu Val Leu Leu Gln Pro Ser Phe Gln Ala
1175 1180 1185

Ser Asp Val Asp Thr Leu Leu Lys Thr Val Leu Pro Ala Val Pro
1190 1195 1200

Ser Asp Pro Ile Leu Val Glu Thr Pro Lys Val Asp Lys Ile Ser
1205 1210 1215

Ser Thr Met Leu His Leu Ile Val Ser Asn Ser Ala Ser Ser Glu
1220 1225 1230

Asn Met Leu His Ser Thr Ser Val Pro Val Phe Asp Val Ser Pro
1235 1240 1245

Thr Ser His Met His Ser Ala Ser Leu Gln Gly Leu Thr Ile Ser
1250 1255 1260

Tyr Ala Ser Glu Lys Tyr Glu Pro Val Leu Leu Lys Ser Glu Ser
1265 1270 1275

Ser His Gln Val Val Pro Ser Leu Tyr Ser Asn Asp Glu Leu Phe
1280 1285 1290

Gln Thr Ala Asn Leu Glu Ile Asn Gln Ala His Pro Pro Lys Gly
1295 1300 1305

Arg His Val Phe Ala Thr Pro Val Leu Ser Ile Asp Glu Pro Leu
1310 1315 1320

Asn Thr Leu Ile Asn Lys Leu Ile His Ser Asp Glu Ile Leu Thr
1325 1330 1335

Ser Thr Lys Ser Ser Val Thr Gly Lys Val Phe Ala Gly Ile Pro
1340 1345 1350

Thr Val Ala Ser Asp Thr Phe Val Ser Thr Asp His Ser Val Pro
1355 1360 1365

Ile Gly Asn Gly His Val Ala Ile Thr Ala Val Ser Pro His Arg
1370 1375 1380

Asp Gly Ser Val Thr Ser Thr Lys Leu Leu Phe Pro Ser Lys Ala
1385 1390 1395

Thr Ser Glu Leu Ser His Ser Ala Lys Ser Asp Ala Gly Leu Val
1400 1405 1410

Gly Gly Gly Glu Asp Gly Asp Thr Asp Asp Asp Gly Asp Asp Asp
1415 1420 1425

Asp Asp Arg Asp Ser Asp Gly Leu Ser Ile His Lys Cys Met Ser
1430 1435 1440

Cys Ser Ser Tyr Arg Glu Ser Gln Glu Lys Val Met Asn Asp Ser
1445 1450 1455

Asp Thr His Glu Asn Ser Leu Met Asp Gln Asn Asn Pro Ile Ser
1460 1465 1470

Tyr Ser Leu Ser Glu Asn Ser Glu Glu Asp Asn Arg Val Thr Ser
1475 1480 1485

Val Ser Ser Asp Ser Gln Thr Gly Met Asp Arg Ser Pro Gly Lys
1490 1495 1500

Ser Pro Ser Ala Asn Gly Leu Ser Gln Lys His Asn Asp Gly Lys
1505 1510 1515

Glu Glu Asn Asp Ile Gln Thr Gly Ser Ala Leu Leu Pro Leu Ser
1520 1525 1530

Pro Glu Ser Lys Ala Trp Ala Val Leu Thr Ser Asp Glu Glu Ser
1535 1540 1545

Gly Ser Gly Gln Gly Thr Ser Asp Ser Leu Asn Glu Asn Glu Thr
1550 1555 1560

Ser Thr Asp Phe Ser Phe Ala Asp Thr Asn Glu Lys Asp Ala Asp
1565 1570 1575

Gly Ile Leu Ala Ala Gly Asp Ser Glu Ile Thr Pro Gly Phe Pro
 1580 1585 1590
 Gln Ser Pro Thr Ser Ser Val Thr Ser Glu Asn Ser Glu Val Phe
 1595 1600 1605
 His Val Ser Glu Ala Glu Ala Ser Asn Ser Ser His Glu Ser Arg
 1610 1615 1620
 Ile Gly Leu Ala Glu Gly Leu Glu Ser Glu Lys Lys Ala Val Ile
 1625 1630 1635
 Pro Leu Val Ile Val Ser Ala Leu Thr Phe Ile Cys Leu Val Val
 1640 1645 1650
 Leu Val Gly Ile Leu Ile Tyr Trp Arg Lys Cys Phe Gln Thr Ala
 1655 1660 1665
 His Phe Tyr Leu Glu Asp Ser Thr Ser Pro Arg Val Ile Ser Thr
 1670 1675 1680
 Pro Pro Thr Pro Ile Phe Pro Ile Ser Asp Asp Val Gly Ala Ile
 1685 1690 1695
 Pro Ile Lys His Phe Pro Lys His Val Ala Asp Leu His Ala Ser
 1700 1705 1710
 Ser Gly Phe Thr Glu Glu Phe Glu Thr Leu Lys Glu Phe Tyr Gln
 1715 1720 1725
 Glu Val Gln Ser Cys Thr Val Asp Leu Gly Ile Thr Ala Asp Ser
 1730 1735 1740
 Ser Asn His Pro Asp Asn Lys His Lys Asn Arg Tyr Ile Asn Ile
 1745 1750 1755
 Val Ala Tyr Asp His Ser Arg Val Lys Leu Ala Gln Leu Ala Glu
 1760 1765 1770
 Lys Asp Gly Lys Leu Thr Asp Tyr Ile Asn Ala Asn Tyr Val Asp
 1775 1780 1785
 Gly Tyr Asn Arg Pro Lys Ala Tyr Ile Ala Ala Gln Gly Pro Leu
 1790 1795 1800
 Lys Ser Thr Ala Glu Asp Phe Trp Arg Met Ile Trp Glu His Asn
 1805 1810 1815
 Val Glu Val Ile Val Met Ile Thr Asn Leu Val Glu Lys Gly Arg
 1820 1825 1830
 Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly Ser Glu Glu Tyr
 1835 1840 1845
 Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val Leu Ala Tyr
 1850 1855 1860
 Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile Lys Lys

1865	1870	1875
Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln Tyr		
1880	1885	1890
His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu		
1895	1900	1905
Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His		
1910	1915	1920
Ala Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg		
1925	1930	1935
Thr Gly Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln		
1940	1945	1950
His Glu Gly Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg		
1955	1960	1965
Ser Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe		
1970	1975	1980
Ile His Asp Thr Leu Val Glu Ala Ile Leu Ser Lys Glu Thr Glu		
1985	1990	1995
Val Leu Asp Ser His Ile His Ala Tyr Val Asn Ala Leu Leu Ile		
2000	2005	2010
Pro Gly Pro Ala Gly Lys Thr Lys Leu Glu Lys Gln Phe Gln Leu		
2015	2020	2025
Leu Ser Gln Ser Asn Ile Gln Gln Ser Asp Tyr Ser Ala Ala Leu		
2030	2035	2040
Lys Gln Cys Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro		
2045	2050	2055
Val Glu Arg Ser Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly		
2060	2065	2070
Thr Asp Tyr Ile Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser		
2075	2080	2085
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Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
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50 55 60
Val Ser Thr Lys Asn Pro Val Arg Thr Val Asn Glu Asn Phe Leu Ser
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Leu Gln Leu Asp Pro Ser Ile Ile His Asp Gly Trp Leu Asp Phe Leu
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Ser Ser Lys Arg Leu Val Thr Leu Ala Arg Gly Leu Ser Pro Ala Phe

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Tyr Ala His Cys Thr Asn His His Asn His Asn Tyr Val Arg Gly Ser
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